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New human obesity protein binding protein-2 homologue nucleic acids, polynucleotides and polypeptides useful for producing medicament for

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is a human obesity protein binding protein-2 homologue (hOB-Bp2h) of the invention. The hOB-Bp2h nucleic acids and polypeptides may be used for the manifacture of a medicament for the treatment of obesity and/or obesity-related disorders. The hOB-Bp2h nucleic acids are
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    leukaemia; allergy; inflammatory
c rhinitis; osteoarthritis; Crohn'
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FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV FKAVTETTKGAPVATNHOSREVEMSTRGRFOLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120

120

60

180 180

240 240

TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGYSAQRTVRLRVAYAPRD

MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW

Conservative

1;

Indels

185;

Gaps

with

acid

61 61

181

LVISISRDNTPD

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CC represent potential markers for screening, diagnosis, prognosis, cc follow-up assays, and imaging methods. (I) is useful as a target for cc drugs which inhibit inflammation, tissue damage and remodeling in cc asthma, and inflammatory diseases such as allergic rhinitts, conjunctivitis, crohn's disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is also useful for monitoring the course of conjunctivitis, etc. (I) is also useful for monitoring the course of cdisease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid conjunctivities (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS (II) are useful as nucleic acid probes are useful for screening genomic (II) are useful as nucleic acid probes are useful for screening genomic clibrary to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS gene copy cumber is determined for detecting diseases or disorders associated with SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also cused to detect, sort or isolate cells expressing SIGLEC-BMS proteins cand in diagnostic imaging technology. AAU87074-AAU87089 represent contains and signostic imaging technology. AAU87074-AAU87089 represent
Query Match
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Matches 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
related lectin) protein (I). Pharmaceutical compositions comprising (I)
are useful for treating immune system diseases such as asthma, leukaemia
or other allergic or inflammatory diseases. Extracellular domains of (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukaemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 11; Figure 6;
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                                                                                  Sequence
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B; ABK43373.
  al Similarity
510; Conserv
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                       95.48;
73.28;
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О
    Score 2580.5; DB 2
Pred. No. 6.9e-196;
1; Mismatches 1;
                                               23;
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ID AAUB
XX AAUB
AC AAUB
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XX Sial
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 The invention relates to an isolated SIGLEC related lectin) protein (I). Pharmaceutical
                                                                                                     Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukaemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; slalic acid-binding Ig-related lectin; SIGLEC; asthma; Immune system disease; leukaemia; allergy; inflammatory disease; tissue damage; allergic thinitis; osteoasthritis; Crohn's disease; psoriasis; rheumatoid arthritis; conjunctivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sialic acid-binding
                                                       Claim 5; Figure 2B; 209pp; English.
                                                                                                                                                                                                                                 Longphre M,
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cc are useful for treating immune system diseases such as asthma, leukaemia cor other allergic or inflammatory diseases. Extracellular domains of (I) crepresent potential markers for screening, diagnosis, prognosis, cc follow-up assays, and inaging methods. (I) is useful as a target for cc drugs which inhibit inflammation, tissue damage and remodeling in cc asthma, and inflammatory diseases such as allergic rhinitis, ccoming the course of cc osteoarthritis, ctc. (I) is also useful for monitoring the course of cc disease or disorders, and for identifying agents that bind with and/or cc modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid cc molecules (II) encoding (I) are useful in diagnosis and/or prognosis cc methods, and to detect the presence and/or amount of SIGLEC-BMS conjunctivities sequences and/or SIGLEC-BMS proteins in a biological sample. (II) are useful as nucleic acid probes are useful for screening genomic clibrary to isolate a genomic clone of SIGLEC-BMS antibodies are also used to detect, sort or isolate calls expressing SIGLEC-BMS proteins coming the conjunctivity of siglec-BMS antibodies are also cused to detect, sort or isolate calls expressing SIGLEC-BMS proteins cand in diagnostic imaging technology. AAU8704-AAU87089 represent
NQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK
                                                                                                                             KRRTQTETPRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK
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75.1%;
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Pred. No. 4.9e-172;
1; Mismatches 1;
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11-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO940 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO; EST; expressed sequence tag; PCR primer; hybridisation; blood coagulation disorder; cancer; cellular adhesion disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
98US-0079920
98US-0080105
98US-0080107
98US-0080165
98US-00801327
98US-0080333
98US-0081070
98US-0081070
98US-00811070
98US-00811071
98US-0081127
98US-0081127
98US-0081127
98US-0081128
98US-008129
98US-008129
98US-0081333
98US-0082569
98US-0082569
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98US-0082569
98US-0082796
98US-0083392
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98US-0083396
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98US-0079656
98US-0079663
98US-0079664
98US-0079689
98US-0079728
98US-0079728
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98US-0040220.
98US-0078886.
98US-0078910.
98US-0078936.
98US-0078939.
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Best Local S
Matches 450
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07-MAY 1998

13-MAY 1998

13-MAY 1998

13-MAY 1998

15-MAY 1998

16-MAY 1998

17-MAY 1998

18-MAY 1998

19-MAY 1998
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29-APR-1998;
29-APR-1998;
29-APR-1998;
29-APR-1998;
30-APR-1998;
05-MAY-1998;
                                                                                       Sequence
                                                                                                                                                                                                                                                                                                Wood
                                                                                                         invention
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                                                                                                                                                                                                                                                                                                                 (GETH )
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DB; AAZ34109.
                                                    450;
                                                            Similarity
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                                                                                      544 AA;
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                  98US-0087208.
98US-0094651.
98US-0100038.
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98US-0084627

98US-0084627

98US-0084640

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98US-0085333

98US-0085573

98US-0085573

98US-0085579

98US-0085597

98US-0085697

98US-0085704

98US-0085697

98US-0085643

98US-0085704

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98US-0083554.
98US-0083558.
98US-0083559.
98US-0083742.
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98US-0084414
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                                                           83.7%;

    Gurney

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Yuan 'n Baker ΚP, Chen Ç

New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -  $\frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{$ 

The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ3891 to AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present

Score 2265; DB 20; Pred. No. 5.2e-171; 1; Mismatches 3; Length Indels 544; 148; Gaps

60 60

61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120

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  08-MAR-1999;
12-MAR-1999;
29-MAR-1999;
21-APR-1999;
21-APR-1999;
14-MAR-1999;
23-JUN-1999;
26-JUL-1999;
26-JUL-1999;
29-OCT-1999;
02-DEC-1999;
02-DEC-1999;
                                                                                                                                                                                                                                    Human; secreted protein; transmembrane protein;
expressed sequence tag; detection; cancer.
                                                                                                                                                                    14-SEP-2000
                                                                                                                                                18-FEB-2000;
                                                                                                                                                                                          WO200053756-A2
                                                                                                                                                                                                                                                                  Human PRO940 (UNQ477) protein sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                      AAB44280 standard;
                                                                                                                                                                                                                sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
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                                                                                                                                                                                                                                                                                                                                                                                                                  512
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                                                                                                                                              2000WO-US04341.
 99US-01310232
99US-0131445
99US-014287
99US-0141037
99US-0145698
99US-0165506
99WO-US28313
99WO-US28551
99WO-US28555
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                                                                                                                                                                                                                                                                                                                                      Protein;
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                                                                                                                                                                                                                                               cytostatic
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Best Local Similarity
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30-DEC-1999;
30-DEC-1999;
30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
06-JAN-2000;
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                     AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bloactive molecules to cells and for modulating blological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bloactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ferrara
Goddard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel PRO polypeptides and polynucleotides used to target bloactive molecules to specific cells, cellular activities -
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Fig 93; 636pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kljavin
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)B; AAC78510.
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GEFTCHARHPLGSOHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP
                                          NIGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
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                                                                                                                                                                                                                                                                               FKAVTETTKGAPVATNHOSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                        LVISISRDNTPD------
                                                                                                                                                                                        TGAALSSQGTKPTTSHESVLSETPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                   FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                                                                           MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                       WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
                                                                                                                                 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
                                                                                                                                                                             -----SFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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Filvaroff E,
Godowski PJ,
Kuo SS, Nap,
Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                     544 AA;
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99WO-US31274.
99WO-US31274.
2000WO-US00219.
2000WO-US00277.
2000WO-US00376.
                                                                                                                                                                                                                                                                                                                                                           Conservative
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74.8%;
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[A, Tumas D,
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Fong S, Gao W, Gerber H, Gerritsen ME;
Grimaldi CJ, Gurney AL, Hillan KJ;
ier MA, Paoni NF, Roy MA;
Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                         Score 2265; DB 21;
Pred. No. 5.2e-171;
1; Mismatches 3;
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14 - MAR - 2000)
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30 - MAR - 2000)
11 - APR - 2000)
25 - APR - 2000)
27 - MAY - 2000)
28 - JUN - 2000)
29 - JUN - 2000)
20 - JUN - 2000)
20 - JUN - 2000)
21 - AUG - 2000)
22 - AUG - 2000)
22 - AUG - 2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200168848-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO
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         2000US-196690P.
2000US-198121P.
2000US-198121P.
2000US-19835P.
2000US-199397P.
2000US-19950P.
2000US-19954P.
2000US-19954P.
2000US-201516P.
2000WO-US13705.
2000WO-US14941.
2000WO-US14941.
2000WO-US14941.
2000WO-US15264.
2000WS-05448484.
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2000US-192655P
2000US-193032P
2000US-193053P
2000US-194049P
2000US-19444P
2000US-194647P
2000US-19600P
2000US-196187P
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2000US-186968P.
2000US-189320P.
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2000US-191048P
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2000WO-US06884
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2000WO-US05841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
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Qy Вþ

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В δÃ

MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW

FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120

120

60 60

ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV Matches

450;

Conservative

1;

Mismatches

Indels 148;

Gaps

Similarity

δÕ Б Qγ Вþ Qy В Qy В Qy 뫄 δÃ

NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE

WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE

LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP

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242 252 182 240 140

TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD

LVISISRDNTPD-----

GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP

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422 390 362 330 302

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Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. CC The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of CC expression of a PRO polypeptide in a test sample of cells from the animal CC and a control sample of normal cells, whereby a higher level of CC expression in the test sample indicates the presence of a tumour in the CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats CC and rabbits but are preferably human. The polypeptides can be used to CC stimulate tumour necrosis factor (TNF) alpha release from human blood, CC when contacted with it. A specific polypeptide can be used to stimulate tumour or differentiation of chondrocyte cells. The PRO CC proteins can be used to determine the presence of tumours and also CC susceptibility to tumour development, particularly adrenal, lung, colon, CC breast, prostate, rectal, cervical, or liver tumours, in mammalian CC subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
     Query Match
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01-DEC-2000;
20-DEC-2000;
                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids encoding PRO polypeptides, used presence of tumours, such as prostate and breast tun to screen for modulators of the compounds -
                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Fig 118; 774pp; English.
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Pan J, Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
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Pred. No. 5.2e-171;
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 16-SEP-1998;
07-OCT-1998;
                                                   02-JUL-2002; 2002US-0188767
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                                                                                                                          US2003036156-A1
                                                                                                                                                               Homo
                                                                                                                                                                                              cartilage disorder;
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450; Conser
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                                                                                                                    KRRTQTETPRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK
                                                                                                                                                                                                                                                                                  GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP
                                                                                                                                                                                                                                                                                                                                                                                                       NIGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
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                                                                                                                                                                                                                                                   GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP
                                                                                                                                                                                                                                                                                                                                                                        NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
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98US-091628P.
98US-091632P.
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   RESULT 9
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AD COMPAND ABU66
AC
AD COMPAND AB
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18-FEB 2000
18-FEB 2000
22-FEB 2000
24-FEB 2000
21-MAR 2000
02-MAR 2000
15-MAR 2000
17-MAY 2000
27-MAY 2000
28-JUL 2000
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21-JUC
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07-OCT-1998;
01-DEC-1998;
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02-DEC-1999;
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01-SEP-1999;
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14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; transmembrane protein; cytostatic;
gene Therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;
adrenal tumour; lung tumour; colon tumour; breast tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC
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98WO-US21141

98WO-US25108

99WO-US205028

99WO-US205111

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99WO-US28331

200WO-US06344

200WO-US05841

200WO-US05841

200WO-US05841

200WO-US14942

200WO-US14941

200WO-US15264

200WO-US32710

200WO-US33287

200WO-US332678

200WO-US316520

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97US-062250P.
97US-063120P.
97US-063120P.
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Matches 450
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16-JUN-1998

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26-JUN-1998

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11-AUG-1998

11-AU
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450; Conserv
               61
                                             μ.
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FKAVTETTKGAPVATNHOSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                           Conservative
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98US-089512P

98US-089514P

98US-08953P

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98US-099653P

98US-090654P

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98US-09699P

98US-097954P

98US-09883P

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98US-09883P
                                                                                                                    83
74
                                                                                                                    . 7%;
                                                                                                 Score 2265; DB 24;
Pred. No. 5.2e-171;
1; Mismatches 3;
                                                                                                      Indels
                                                                                                                                Length
                                                                                                    148;
                                                                                                    Gaps
                 120
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28-OCT 1997
31-OCT 1997
31-OCT 1997
31-OCT 1997
24-NOV 1997
24-NOV 1997
21-NOV 1997
11-DEC 1997
11-DEC

97US-063564P 97US-063734P 97US-064103P 97US-066466P 97US-066466P 97US-066466P 97US-066975P 97US-069425P 97US-069425P 97US-06907P 97US-06907P 97US-06907P 97US-077450P 98US-077450P 98US-080107P 98US-080107P 98US-081050P 98US-081950P 98US-081950P 98US-084440P 98US-08459P 98US-08459P 98US-08459P 98US-08459P 98US-084692P 98US-084692P 98US-084692P 98US-08539P 98US-08539P 98US-086033P 98US-086392P 98US-088028P 98US-088028P 98US-088028P 98US-088028P 98US-088028P 98US-088028P 98US-088028P 98US-088028P 98US-088028P 98US-088117P 98US-088811P 98US-088815P 98US-088815P 98US-088815P 98US-088815P 98US-088825P 98US-088825P 98US-088825P 98US-088825P 98US-088825P 98US-088825P 98US-088825P 98US-088825P 98US-088825P 98US-088825P

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RESULT 10
ABUG7464
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Wood WI, Zhang Z; Gurney AL;

2003-332039/31. DB; ACA05758.

New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, in chromosome and gene mapping, as chromosomarkers, in tissue typing, and in chromosome identification chromosome

Claim 11; Fig 118; 706pp; English.

The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides. Also disclosed is an antibody that specifically binds to the PRO polypeptide, a method for stimulating trelease of tumour necrosis factor alpha (TNF-alpha) from human blood contacting the blood a PRO polypeptide, a method for stimulating the the d by

wound healing;

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05-JAN-1999;
08-MAR-1999;
10-MAR-1999;
14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-1998;
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2000WO-USO0277
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2000WO-USO6319
2000WO-USO641941
2000WO-USO64194
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2000WO-USO6710
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polypeptides, and the polynucleotide sequences encoding them. The CC PRO polypeptides are useful for detecting other PRO polypeptides, for CC polypeptides are useful for detecting other PRO polypeptides, for CC linking bloactive molecules to cells expressing PRO polypeptides, CC for modulating biological activities of cells expressing PRO polypeptides, CC polypeptides, and for for identifying agonists or antagonists. The CC polypeptides are useful for the cell. The PRO polypeptides are useful for treating immune disorders, diabetes or hyper- or hypo-insulinaemia, CC cardiac insufficiency nervous system disorders, kidney disorders, CC thousand cartilage disorders or arthritis, tumours, and wound healing. CC The polypucted sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation CC contains transgenic animals or knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy. ABU61071-ABU61164 represent the human PRO polypeptides of the
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Goddard
Kljavin
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                                                                                                                                                                                                                                                                                                                 Claim 12; Fig 93; 459pp; English.
                                                                                                                                                                                                                                                                                                                                            Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies
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19-JUN-2001;
                                                                                                                                                                                                                                           present invention relates to the isolation of novel human PRO ypeptides, and the polynucleotide sequences encoding them. The polypeptides are secreted and transmembrane proteins. The PRO ypeptides are useful for detecting other PRO polypeptides, for
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99US-0380137.
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f E, Fong S, Gao W, Ger
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TA, Tumas D, Williams F
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                                                                  Human; PRO; cytostatic; chromosome mapping; gene mapping; protein electrophoresis; tumour necrosis factor-alpha; TNF-alpha; chondrocyte differentiation; chondrocyte proliferation; tumour.
                                                  Homo
                             US2003032102-A1
                                                                                                             Human PRO polypeptide #59.
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                                                                                                               WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
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98US-096867P

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98US-091359P.
98US-091544P.
98US-091478P.
98US-091486P.
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Pred. No. 5.2e-171;
1; Mismatches 3;
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28-JUL-2000;
24-AUG-2000;
08-NOV-2000;
10-NOV-2000;
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28-FEB-2001;
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29-JUN-2001;
09-JUL-2001;
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10-MAR-1999
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07-OCT-1998;
01-DEC-1998;
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2000WO-US20710.
2000WO-US23328.
2000WO-US330952.
2000WO-US330873.
2000WO-US34956.
2001WO-US45520.
2001WO-US17800.
2001WO-US17800.
2001WO-US17803.
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99WO-USO5190
99WO-US10733
99WO-US10733
99WO-US20111
99WO-US21990
99WO-US28301
99WO-US28301
99WO-US28301
99WO-US31274
2000WO-US04341
2000WO-US04341
2000WO-US04341
2000WO-US04341
2000WO-US04341
2000WO-US05601
2000WO-US05604
2000WO-US05604
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98WO-US25108
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    97US-059263P

97US-062250P

97US-062250P

97US-063140P

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97US-0631544P

97US-063154P

97US-063154P

97US-063154P

97US-0664103P

97US-0664103P

97US-0664103P

97US-0664103P

97US-0664120P

98US-077632P

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                                                                                          Query Match
Best Local Similarity
Matches 450; Conserv
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10-JUN-1998
110-JUN-1998
110-JUN-1998
110-JUN-1998
111-JUN-1998
111-JUN
      Conservative
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980S-088874P

980S-088861P

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980S-090560P

980S-090560P

980S-090560P

980S-091638P

980S-091638P
                        83.7%;
74.8%;
  Score 2265; DB 24;
Pred. No. 5.2e-171;
1; Mismatches 3;
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      Indels
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10-SEP-1998;
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                                                                                                                                                                       Homo
                                                                                                                                                                                                       tumour; adrenal tumour; lung tumour; colon tumour; breast tumour;
prostate tumour; rectal tumour; cervical tumour; liver tumour;
bone disorder; cartilage disorder; arthritis; sports injury.
                                                                                                                                                                                                                                                     Human; secreted protein; transmembrane protein; PRO; antiarthritic; vulnerary; tumour necrosis factor-alpha; chondrocyte cell proliferation; chondrocyte cell differentiation;
                                                                                                                                                                                                                                                                                                                              Human secreted/transmembrane protein, PRO940.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
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                                                            2002US-0176913
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
         97WO-US20069
98WO-US18824
                                                                                                                                                                                                     cartilage disorder; arthritis; sports injury.
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   21-MAR-2000

30-MAR-2000

17-MAY-2000

22-MAY-2000

23-MAY-2000

28-JUL-2000

21-AUG-2000

24-AUG-2000

24-AUG-2000

20-DEC-2000

10-NOV-2000

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20-DEC-2000

21-MAY-2001

22-MAY-2001

22-MAR-2001

23-MUG-2001

24-AUG-2001

25-MAY-2001

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14-MAY-1999;
02-JUN-1999;
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01-DEC-1998;
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08-MAR-1999;
99WO-US0110.
99WO-US0110.
99WO-US0110.
99WO-US0111.
99WO-US20111.
99WO-US20944.
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99WO-US2072.
2000WO-US0684.
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Best Local Sim
Matches 450;
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11-JUN-1998
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                                                                                      NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                                                                                      NQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK
                            KRRTQTETPRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK
                                                                                                                                                         LVISISRDNTPD
                                                                                                                                                                             ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
||||||| || ||||||
                                                                                                                    WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
                                                                                                                                                LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
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98US-089514P.
98US-089538P.
98US-089538P.
98US-089553P.
98US-08952P.
98US-090252P.
98US-090252P.
98US-090445P.
98US-090445P.
98US-090444P.
98US-09064P.
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98US-088876P.
98US-089090P.
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74.88;
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; Pred. No. 5.2e
1; Mismatches
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5.2e-171;
es 3;
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11-DEC 1998
11-MAR 1998
11-MAR 1998
11-MAR 1998
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23-MAY 1998
24-JUN 1998
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28-MAY 1998
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20-JUN 1998
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21-JUN 1998

97US-063541P.
97US-063344P.
97US-063344P.
97US-063334P.
97US-065311P.
97US-066120P.
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97US-066120P.
97US-069870P.
97

S-088202P S-088212P S-088212P S-088655P S-088734P S-088740P S-088740P S-088824P S-088825P S-088825P S-088825P S-088825P S-088825P

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RESULT 15
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XX ABU56
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XX Chond
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     98WO-US19330.
98WO-US21141.
98WO-US21109.
99WO-US20511.
99WO-US20511.
99WO-US2051.
99WO-US2051.
99WO-US2051.
99WO-US2051.
99WO-US2031274.
2000WO-US0444.
2000WO-US0444.
2000WO-US05841.
2000WO-US05841.
2000WO-US05841.
2000WO-US05841.
2000WO-US11042.
2000WO-US11042.
2000WO-US11042.
2000WO-US12735.
2000WO-US23328.
2000WO-US23328.
2000WO-US23495.
2000WO-US25691.
2000WO-US2569.
2001WO-US2569.
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97US-063734P

97US-063734P

97US-0664103P

97US-066120P

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97US-0669079

97US-0680779

97US-0680779

97US-0680779

97US-068017P

98US-077643P

98US-077643P

98US-077643P

98US-077643P

98US-080137P

98US-080194P

98US-08104P

98US-084640P

98US-084640P

98US-08463P

98US-08632P

98US-08632P

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Matches 450; Conserv
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61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQVFFRV 120
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                                                              83.7%;
milarity 74.8%;
Conservative
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98US-090695P

98US-091110P

98US-091110P

98US-091128P

98US
                                                                                                                                                Score 2265; DB 24;
Pred. No. 5.2e-171;
1; Mismatches 3;
                                                                                                                                                                                     Length
                                                                                                                                                   Indels 148;
                                                                                                                                                                                            544;
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Qy ·	Qy Qb	Qу	Qу Db	Qy Db	Qу	Qy	Дb	Qy Db
511 FQ 512 .    543 FQ 544	451 NQKKQYQLPSPPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK	391 KRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK 	331 GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP	271 NIGNGTSLPYLEGOSICLYCYTHSSPPARLSWTQRGQYLSPSQPSDDGYLELPRYQYEHE	253	241 LVISISRDNTPD	181 TGAALSSQGTKPTTSHFSVLSFTPRPODHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD	61 FRAVIETYKGAFVATNHØSKEVEMSTRGKFØLIGDPAKGNCSLVIKDAQMØDESQYFFRV 120 121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180 [                     121 ERGSYVTYNFMNDGFFLKVT
			LIIMKILP         LIIMKILP	PRVQVEHE        PRVQVEHE	QANRTVLE	RVLSSSHP		CPPPSFSW
	510 542	450 482	390 422	330 362	270 302	252 242	240 182	120 180 140

Search completed: October Job time : 58 secs 8 2003, 20:01:58

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Result
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match Length
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Gapop 10.0 , Gapext 0.5
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Listing first 45 summaries
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differentiation an
CD22 homolog/B lym
B-cell adhesion pr
B-cell adhesion pr
billary glycoprote
                                                        transmembrane carc pregnancy-specific heparan sulfate pr advanced glycosyla nephrin - human pregnancy-specific vascular cell adhe
         vascular cell adhe hypothetical prote hemicentin precurs myosin-light-chain
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biliary glycoprote
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Schwann cell myeli
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m33-B isoform - mo
                                                                                                                                                                                                                                probable advanced
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A; Residues: 1-364 <SIM>
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Best Local Similarity
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45	44	43	42	41	40	39	38	37	36	35	34	ယ	32	31	30
138	138.5	. 138.5	139	139.5	140	140	140.5	140.5	140.5	140.5	141	141.5	142.5	143	144.5
5.1	5.1	5.1	5.1	5.2	5.2	5.2	5.2	.5.2	5.2	5.2	5.2	5.2	5	5. 3	5.3
324	495	349	404	419	628	521	428	428	417	392	402	739	1232	702	26926
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G43354	A55181	A34815	161596	JC4123	138000	S34338	157486	JS0032	RWHUPA	RWHUPD	A54312	JN0581	T43027	A36319	I38344
pregnancy-specific	pregnancy-specific	carcinoembryonic a	advanced glycosyla	pregnancy-specific	Lutheran blood gro	biliary glycoprote	pregnancy-specific	pregnancy-specific	poliovirus recepto	poliovirus recepto	pregnancy-specific	vascular cell adhe	neural cell adhesi	carcinoembryonic a	titin, cardiac mus

A;Gene: GDB:CD33
A;Gene: GDB:CD33
A;Gene: GDB:CD33
A;Gross-references: GDB:119762; OMIM:159590
A;Map position: 19q13.3-19q13.4
C;Superfamily: immunoglobulin homology
C;Keywords: glycoprotein; surface antigen; transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;1-17/Domain: extracellular #status predicted <EXTS>
F;260-282/Domain: transmembrane #status predicted <CYTS>
F;283-364/Domain: intracellular #status predicted <CYTS>
F;100,113,160,209,230/Binding site: carbohydrate (Asn) (covalent) #status predicted myeloid cell surface antigen CD33 precursor - human C;Species: Homo sapiens (man) C;Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 J. Immunol. 141, 2797-2800, 1988
A;Title: Isolation of a cDNA encoding CD33, a differentiation antigen of myeloid A;Reference number: A30521; MUID:89009814; PMID:3139766
A;Accession: A30521 248 61 FREGAIISGDSPVATNKLDQEVQEETQGRFRLLGDPSRNNCSLSIVDARRRDNGSYFFRM 120 61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240 SWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLIS LVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARL LSAAPTSLG--PRTTHSSYLIITPRPQDHGTNLTCQVKFAGAGYTTERTIQLNYTYVPQN ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180 ERGS-TKYSYKSPQLSVHVTDLTHRPKILIPGTLEPGHSKNLTCSVSWACEQGTPPIFSW -SGKQETRAGVV--25.6%; Score 694; DB 2; Length 364; 32.8%; Pred. No. 4.3e-40; tive 59; Mismatches 137; Indels 148; ALIGNMENTS 01-Dec-1989 #text\_change 29-Aug-1997 Gaps 300 179 247 8 prog

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A;Status: not comp.

A;Status: not comp.

A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-626 <SPA>
R;Sato, S;; Fujita, N.; Kurihara, T.; Kuwano, R.; Saklmu...,
R;Sato, S;; Fujita, N.; Kurihara, T.; Kuwano, R.; Saklmu...,
Biochem. Biophys. Res. Commun. 163, 1473-1480, 1989
Biochem. Biophys. Res. Commun. 163, 1473-1480, 1989
A;Title: cDNA cloning and amino acid sequence for human myelin-associated
A;Title: cDNA cloning and amino acid sequence for human myelin-associated
                                                                                                                                                                                                                                                                         myelin-associated glycoprotein precursor - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 16-Aug-1996 #text_change 29-Oct-1999
C;Accession: A61084; A33263; PC2011
R;Spagnol, G; Williams, M.; Srinivasan, J.; Golier, J.; Bauer, D.; Lebo, R.V.;
J. Neurosci. Res. 24, 137-142, 1989
A;Title: Molecular cloning of human myelin-associated glycoprotein.
A;Reference number: A61084; MUID:90064604; PMID:2479762
A;Accession: A61084
A;Status: not compared with conceptual translation
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A:Title: Molecular cloning of two isoforms
A:Reference number: I52590; MUID:94250900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       m33-B isoform - mouse
C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
C:Accession: I52590
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Pred. No. 1.1e-28;
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A;Map position: 19913.1-19913.1
C;Superfamily: myelin-associated glycoprotein; immunoglobulin homology
C;Superfamily: myelin-associated glycoprotein; phosphoprotein; transmemb
F;1-19/Domain: signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;0-626/Product: myelin-associated glycoprotein #status predicted <MAT>
F;35-102/Domain: immunoglobulin homology <IMN>
F;318-120/Region: cell attachment (R-G-D) motif
F;514-536/Domain: transmembrane #status predicted <TMM>
F;914-536/Domain: transmembrane #stat
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A;Accession: A3263
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Mosidues: 1-613,'T',615-626 <SAT>
A;Cross-references: GB.M29273; NID:g187292; PIDN:AAA59545.1;
A;Cross-references: GB.M29273; NID:g187292; PIDN:AAA59545.1;
B;Burger, D.; Pidoux, L.; Steck, A.J.
Blochem. Biophys. Res. Commun. 197, 457-464, 1993
A;Title: Identification of the glycosylated sequons of human
A;Reference number: PC2011; MUID:94092116; PMID:7505568
A;Accession: PC2011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;573/Binding site: phosphate (Ser) (covalent) #status predicted
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Best Local
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137; Conser
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                                                                                                                                                                                                                                                                                                                                                           HCAAARDTVQCLCVVKSNPEPSVAFELPSRNVTVNESEREFVYSERSGLVLTSILTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKEKQILSTVIYESELQLELPAVSPEDDGEYWCVAENQYGQRATAFNLSVEFAPVLLLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIVEMNSSVEATEGSHVSLLCGADSNPPPLLTWMRDGTVLREAVAESLLLELEEVTPAED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFSEH----SVLDIVNTPNIVVPPEVVAGTEVEVSCMVP---DNCPELRPELSWLGHEGL
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Pred. No. 3.5e-13;
0; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                    -STAF----
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d <SIG>
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23;

protein

expe

glycop

C;Genetics:	Db 463 PPGSDGSITGI-LTLRGPLEPRLLVLCAARNRHGTTAROLRFHHPGGLVWAK 513
C;Comment: The long form predominates in early postnatal life; alternative splicing p C;Comment: The papers cited variously predict the mature protein to begin at residue	SNOAFDGIGITALLELCHALIMKIDE
A;Cross-references: GB:MLI/21; NID:g206/80; PIDN:AAA42082.1; PID:g206/81 C;Comment: The sequence contains five presumably extracellular domains that are dista	403 SENISVETPENLEASKCIAGGDGVKCVCMVNSIPDSSEVFEELPTRNQTVSDGHRDFTAA
A; Residues: 'KS', 311-626 < RE2>	
A:Status: preliminary; translated from GB/EMBL/DDBJ	Ov 347 SLSLSVHYKKGLI
A;Reference number: 152892; MUID:842065//; PMID:6586369 A;Accession: I52892	Db 343 SYTCRAESEPAAILTVLRGGKVMAAAIYEDHVTMEMRPARPEDGGTYSCVAENQHGASST 402
A;Title: Cellular localization and function of the proteins encoded by brain-specific	WTQRGQVLSPSQPSDPGVLELPRVQVEHEG
R;Sutcliffe, J.G.; Milner, R.J.; Bloom, F.E.	Db 284 GRNLRLLLSNVGPDDGGSFSCVAENRHGRHNRSLQLRVAYAPRAPVING-SLWVVSGDPV 342
A;Residues: 'KS',311-626 <res> A;Cross-references: GB:M36702; NID:q203181; PIDN:AAA40831.1; PID:q203182</res>	Oy
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA	Db 224 SLSFQADVGLDVQYEPQVVGLWGPTEVVEGSDVELGCEAEGRPAPLISWFRGSEVLREEP 283
A;Reference number: I56564; MUID:85263773; PMID:4020419 A;Accession: I56564	223
J. Neurosci. 5, 1781-1802, 1985 A; Title: Immunocytochemical mapping of 1B236, a brain-specific neuronal polypeptide of the control	104 CFFLRFLLTWTGTEELLDFIGKERIEDDLGSKSLLGSLRFRFRKEDLGRRVGCGVTFINS
A;NOTE: the authors translated the codon CAG for residue 350 as Asn R;Bloom, F.E.; Battenberg, E.L.F.; Milner, R.J.; Sutcliffe, J.G.	1/3 CPY - PSESWIGA - ALSSQGIK PTISHESVESETPREQUEDIDETCHYDESKK
A;Cross-references: GB:V01544; GB:J00756; NID:g56879; PIDN:CAA24786.1; PID:g818027 A;Experimental source: clone p1B236	111 AGKYYFRGDLGGYNQYSF-SEHAELDVWAAPHLEVPHELVAGSEAEILCRVPDN
A;Molecule type: mRNA A;Residues: 'KS',311-626 <sut></sut>	114 -SQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEE
PMID: 6347394	59FGSPYPKNYPPVVARSRPSSAVHESFAGRASFLGDPTGRDCTLNIARLSEEL
Cell 33, 671-682, 1983  A; Title: Identifying the protein products of brain-specific genes with antibodies to	Qy
A;Cross-references: GB:X05301; NID:g56611; PIDN:CAA28920.1; PID:g56612 R:Sutcliffe, J.G.; Milner, R.J.; Shinnick, T.M.; Bloom, F.E.	/LLMGTGCISAPWAAWMPPKMAALSGTCVQLPCRFDYPEELRPASIGGLW
A; Molecule type: mRNA A; Residues: 1-626 <sal></sal>	Qy 5 LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFK 62
A; Reference number: A27185; MUID:87166195; PMID:2435742 A; Accession: A27185	8; Conservative 89;
J. Cell Biol. 104, 957-965, 1987  A:#itle: The amino acid sequences of the mobile-associated glycoproteins: homology to	Query Match 11.2%; Score 302.5; DB 2; Length 620; Best Local Similarity 22.4%; Pred. No. 4.7e-13;
A;Cross-references: GB:M14871; NID:g205267; PIDN:AAA41556.1; PID:g205268 B:Saliger T V. Holmos W D . Colman D D	F;222,314,331,405,449/Binding site: carbohydrate (Asn) (covalent) #status predicted
A; Molecule type: MRNA A: Bookdang 1505 (ARNA A: Bookdang 1505 (ARNA	
A;Reference number: A94175; MUID:87092455; PMID:2432614	F:18-620/Product: Schwann cell muelin proteinted <sig></sig>
Proc. Natl. Acad. Sci. U.S.A. 84, 600-604, 1987  A.T.   P. M. Acad. Sci. U.S.A. 84, 600-604, 1987  A.T.   P. M. Acad. Sci. U.S.A. 84, 600-604, 1987	ogy
A;Cross-references: GB:M16800; NID:g205269; PIDN:AAA41557.1; PID:g205270  R:Aronint M: Poder T: Chia I.S: Down T: Wilkinson D: Bayley M: Braun D	C hearn
A; MoLecule type: mRNA A: Rosidines: 1-606 (LAT)	A; Accession: PS0356 A; Molecule type: protein
A;Reference number: A29028; MÜID:87232001; PMID:2438699	,
Proc. Natl. Acad. Sci. U.S.A. 84, 4337-4341, 1987 A;Title: Two forms of 1B236/myelin-associated qlycoprotein, a cell adhesion molecule	A;Residues: 1-620 <dul> A;Cross-references: GB:S83711; NID:g245729; PIDN:AAB21466.1; PID:g245730</dul>
C;ACCession: A29028; A94175; A27185; A90836; I56564; I52892; A03138; A26362 R;Lai, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner,	A; Molecule type: mRNA
	A;Title: Molecular characterization of the schwann cell myelin protein, SMP: structural A;Reference number: JH0593; MUID:92153423; PMID:1739462
myelin-associated glycoprotein precursor, long splice form - rat N;Alternate names: 1B236; brain neuron cytoplasmic protein 3; MAG	.; Rossier, J
	JH0593; PS0356
7 E.111360	in the second of
Db 574 GAMERWALGVKEGSGAPQEVTPTSHPPMKPTRGPLEDPPEYAEIR 618	Cell myella protein procurage - Tereposo
Qy 453KKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510	RESULT 4
Db 514 VGPVGAVVAFAIVIAVVCYLSQSRRKKGAGSPEVTPVQPMAGPGGDPDLDLRPQQVRWLR 573	Db 587RGEPPELDLSYSHSDL-GKRPTKDSYTLSEELAEVAEIR 624
Qy 407STILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQ 452	Qy 462 PEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510

A; Gene: MAG

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Ision 31-Dec-1989 #text_change 01-Dec-2000
85; A90836; I56564; I52892; A03138; A26362
; NOTONha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner,
4337-4341, 1987
n-associated glycoprotein, a cell adhesion molecule
87232001; PMID:2438699
                                                   D:9203181; PIDN:AAA40831.1; PID:9203182
Bloom, F.E.
Ol. 48, 477-484, 1983
d function of the proteins encoded by brain-specific 84206577; PMID:6586369
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.S.; Down, J.; Wilkinson, D.; Bayley, H.; Braun, P., 600-604, 1987
imary structure of myelin-associated glycoprotein. 87092455; PMID:2432614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :J00756; NID:g56879; PIDN:CAA24786.1; PID:g818027
36
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man, D.R.
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                                                                                                                                                                                                                                                                                                                    ng of 1B236, a brain-specific neuronal polypeptide (
35263773; PMID:4020419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D:g56611; PIDN:CAA28920.1; PID:g56612
Shinnick, T.M.; Bloom, F.E.
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from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                    codon CAG for residue 350 as Asn
Milner, R.J.; Sutcliffe, J.G.
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RESULT 6
BNRP13S
myelin-associated glycoprotein precursor, short spince
N;Alternate names: 1B236; brain neuron cytoplasmic prot
C;Species: Rattus norvegicus (Norway rat)
C;Jate: 30-Jun-1990 #sequence_revision 30-Jun-1990 #te
C;Accession: B29028; B27185; A60055
C;Accession: B29028; B27185; A60055
R;Lai, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Qua-
R;Lai, C.; Brow, Sci. U.S.A. 84, 4337-4341, 1987
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C:Superfamily: myelin-associated glycoprotein; immunoglobulin homology
C:Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein; trans
F:1-19/Domain: signal sequence #status predicted <STG>
F:0-626/Product: myelin-associated glycoprotein, long splice form #status predicted <M#
F:35-102/Domain: immunoglobulin homology <IMM1>
F:118-120/Region: cell attachment (R-G-D) motif
F:152-219/Domain: immunoglobulin homology <IMM2>
F:254-307/Domain: immunoglobulin homology <IMM3>
F:340-394/Domain: immunoglobulin homology <IMM5>
F:340-394/Domain: immunoglobulin homology <IM5-
F:340-394/Domain: immunoglobulin homology <IM5-
F:340-340-340-
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:337-636/Domain: intracellular #status predicted <INT>
:99,223,246,315,332,406,450,454/Binding site: carbohydrate (Asn) (covalent)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SILTLRGQAQAPPRVICTSRNLYGT-QSLELPFQGAHRLMWAKIGPVGAVVAFAILIAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIYACLAENAYGQDNRTVELSYMYAPWKPTVNGTVVAV-EGETVSILCSTQSNPDPILTI
                                                                                                                                                                                                                                                                                                RGEPPELDLSYSHSDL-GKRPTKDSYTLTEELAEYAEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                          ---PSPESKKNQKKQYQLPSF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVVPTAGP-----LAQKRNQKATPNSPRTPL-----PPGA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCAAARDTV-----QCLCVVKSNPEPSVAFELPSRNVTVNETEREFVYSERSGLL-LT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSNGAFLGIGITALLFLCLALI-----IMKILPKRR-TQTETPRP-RFSRHSTILDYI 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKEKQILATVIYESQLQLELPAVTPEDDGEYWCVAENQYGQRATAFNLSVEFAPIILLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEPTVLGRLREDEGTWVQVSLLHFVPTREANGHRLGCQAAFPNTTLQFEGYASLDVKYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQGT-----KPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFSEH----SVLDIINTPNIVVPPEVVAGTEVEVSCMVP---DNCPELRPELSWLGHEGL
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Pred. No. 1.4e-12;
5; Mismatches 239;
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                                                                                                                                                      or, short splice cytoplasmic prot
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                                                           Quarles,
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                                                        R.H.; Bloom, F.E.;
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                                                      Milner,
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F;514-536/Domain:
F;537-582/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Cell Biol. 104,
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                                                           FKEKQILATVIYESQLQLELPAVTPEDDGEYWCVAENQYGQRATAFNLSVEFAP-----
                                                                                                     TQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLISTA
                                                                                                                                                      GIYACLAENAYGQDNRTVELSVMYAPWKPTVNGTVVAV-EGETVSILCSTQSNPDPILTI
                                                                                                                                                                                                                                                 VIVEMNSSVEAIEGSHVSLLCGADSNPPPLLTWMRDGMVLREAVAESLYLDLEEVTPAED
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                                                                                                                                                                                                  --MVSOANRTV-----LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSW
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64;

-RDNTPDP

-PENLRY--

300 259 240 238 180 186 Pred. No. 3.3e-12;
4; Mismatches 185;

Indels 115;

Gaps

89 67

128

.3e-1

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C;Superfamily: myelin-associated glycoprotein; immunoglobulin homology
C;Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein;
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-582/Product: myelin-associated glycoprotein, short splice form #status predict
F;35-102/Domain: immunoglobulin homology <IMM1>
F;118-120/Region: cell attachment (R-G-D) motif
F;152-219/Domain: immunoglobulin homology <IMM2>
F;254-307/Domain: immunoglobulin homology <IMM4>
F;254-307/Domain: immunoglobulin homology <IMM4>
F;45-490/Domain: immunoglobulin homology <IMM5>
F;450-399/Domain: immunoglobulin homology <IMM5>
F;450-90/Domain: immunoglobulin homology <IMM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Comment: The sequence contains five C:Comment: The short form is found in C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 419-582 (SAL)
A;Cross-references: GB:X06554; NID:g56614; F
R;Tropak, M.B.; Johnson, P.W.; Dunn, R.J.; F
Brain Res. Mol. Brain Res. 4, 143-155, 1988
A;Title: Differential splicing of MAG transon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 565-582 <TRO>
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A; Accession: A60055
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A; Residues: 1-582 <LAI>
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A;Accession: B29028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M22357; NID:g205271; R;Salzer, J.L.; Holmes, W.P.; Colman, D.R.
                                                          ,246,315,332,406,450,454/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holmes, W.P.; Co. 04, 957-965, 1987
                                                                                             transmembrane #status predicted intracellular #status predicted
10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of MAG transcripts during CNS
Score 289.5;
Pred. No. 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 presumably the adult;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN:CAA29797.1;
Roder, J.C.
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                       DB 1;
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myelin-associated glycoprotein - mouse
C;Specles: Mus musculus (house mouse)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 23-Jul-1999
C;Accession: B33785; A33785; S05687; S02374
R;Fujite, N; Sato, S.; Kurihara, T; Kuwano, R; Sakimura, K.; Inuzuka, T.; Takahashi, Biochem. Biophys. Res. Commun. 165, 1162-1169, 1989
A;Title: cDNA cloning of mouse myelin-associated glycoprotein: a novel alternative splid R;Reference number: A33785; MUID:90121220; pMID:2482022
A;Accession: B33785
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Superfamily: myelin-associated glycoprotein; immunoglobulin C:Keywords: alternative splicing; glycoprotein; transmembrane F:152-219/Domain: immunoglobulin homology <IMM2>
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A; Molecule type: mRNA
A; Residues: 310-374;566-582 <FU4>
A; Cross-references: EMBL:X07849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 310-374; 566-573, 584-588
A; Cross-references: EMBL: X07849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Developmentally regulated alternative splicing of brain myelin-associated A;Reference number: S02374; MUID:88242820; PMID:2454205 A;Accession: S05887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M31811; NID:g199016; PIDN:AAA39487.1; PID:g199017 R;FUJita, N.; Sato, S.; Kurihara, T.; Inuzuka, T.; Takahashi, Y.; Miyata FEBS Lett. 232, 323-327, 1988
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A; Residues: 1-582 <FU3>
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A; Residues: 1-637 <FUJ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FWIRVQES------VMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTETT
                                                                                                                                                                                                                                            GEPTVLGRLREDEGTWVQVSLLHFVPTREANGHRLGCQAAFPNTTLQFEGYASLDVKYPP
                                                                                                                                                                                                                                                                                                                            TFSEH----SVLDIVNTPNIVVPPEVVAGTEVEVSCMVP---DNCPELRPELSWLGHEGL
                                                                                                                                                                                                                                                                                                                                                                     NEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPP--PSFSWTGAALS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRY 128
LTIFKEKQILATVIYESQLQLELPAVTPEDDGEYWCVAENQYGQRATAFNLSVEFAP---
                                      LSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLI 359
                                                                               GVYACLAEN - - - AYGQDNRTVELSVMYAPWKPTVNGTVVAV - EGETVSILCSTQSNPDPI
                                                                                                                                                             VIVEMNSSVEATEGSHVSLLCGADSNPPPLLTWMRDGMVLREAVAKSLYLDLEEVTPGED
                                                                                                                                                                                                     RDLVISIS------RDNTPDP-----
                                                                                                                                                                                                                                                                                   SQGT-----KPTTSHESVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FWIMISASRGGHWGAWMPSTISAFEGTCVSIPCRFDFP--DELRPAVVHGVWYFNSPYPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                    --PENLRYMYSQANRTY-----LENLGNGTSLPVLEGQSLCLVCVTHSSPPAR
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Pred. No. 4.4e-12;
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               C; Genetics:
A; Gene: CD2:
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$1310adhesin - mouse
$150065
$1310adhesin - mouse
$150065
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                                                                                                               J. Immunol. 151, 175-187, 1993
A;Title: Organization of the murine Cd22 locus. Mapping A;Reference number: 149583; MUID:93315834; PMID:8100843
A;Accession: 149583
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                       differentiation antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                          RESULT
I49583
                                                                           A; Molecule type: mRNA
A; Residues: 1-862 < RES>
                                                                                                                                                                                                                       R; Law, C.
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A;Molecule type: mRNA
A;Residues: 1-1694 <CRO>
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                                                     A;Cross-references: GB:L16928; NID:g348965; PIDN:AAA02562.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                LSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVS-LSLSVHY
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25.7%;
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PMID:7925291
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character

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RESULT 10
A46512
CD22 homolog/B lymphocyte-restricted adhesion molecule - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C;Accession: A46512
R;Torres, R.M.; Llaw, C.L.; Santos-Argumedo, L.; Kirkham, P.A.; Grabstein, K.; Parkhouse, J. Immunol. 149, 2641-2649, 1992
A;Title: Identification and characterization of the murine homologue of CD22, a B lymphod A;Reference number: A46512; MUID:93017867; PMID:1401903
A;Accession: A46512
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-868 <TOR>
A;Residues: 1-868 <TOR>
A;Experimental source: B cell lymphoma 38C13
A;Note: sequence extracted from NCBI backbone (NCBIP:116156)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 DKATKKFKGT-VLYNKAEPELYPPKQRRVTFLGN-SIDNCTLKIHPIRANDSGNLGLRMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                Similarity
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NVYTESKLTFQPKWTDHGKSVKCQVQHSSK-VLSECTVHLDVKYTPKLEIKVNPTEVEKN
                                     SHF--SVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAP---
                                                                                                                                                                            TRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQK 145
                                                                      PYIOMPSEIRESQSVTLTCGLNFSCFGYDILLKWFLEDSEITSITSSVTSITSSVTSSIK 212
                                                                                                       PDVYIPETLEPGOPVTVICVFN------WAFEECPPPSFSWTGAALSSQGTKPTT 194
                                                                                                                                           KQGRVTFLGNRI-DNCTLKIHPIRANDSGNLGLRMTAGT----ERWMEPIHLNVSEKPFQ
                                                                                                                                                                                                               EGACIRIPCKYKTPLPKARLDNILLFQNYEFDKATKKFTGTCLYNATKTEKDPESELYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGSQHV--SLSLSVHYKKGLISTAFSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQSVELICESLASPSATNYTWYHNRKPI----PGDTQEKLRIPKVSPWHAGNYSCLAENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQSLCLVCVTHSSPPA-RLSWTQRGQVLSPSQPSD-PGVLELPRVQVEHEGEFTCHARHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -QEQQMSKLILHSVTKDMRGKYRCQASNDIGPGESEEVELTVHYAPEPSRVHIYPSPAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VMVSQANRTVL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVRLDVKYTPKLEIKVNPTEVEKNNSVTMTCRVNSSNPKLRTVAVSWFKDGRPLEDQELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGT----ERWMEPIHLNVSEKPFQPYIQMPSEIRESQSVTLTCGLNFSCFEYDILLQWFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDSKITSVTPSVTSITSSVTSSIKNVYTESKLTFQPKWTDHGKSVKCQVQHSSE-VLSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLILGHAASAQYSSANDWTVDHPQTLFAWEGACIRIPCKYKTPLPKARLDNILLFQNYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLSSLLGGSQAMDGRFW-IRVQESVMVPEGLCISVPCSFS--YPRODWTGSTPAYGYWF
                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                        8.1%; Score 220.5;
21.7%; Pred. No. 2.8;
ative 57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 227; DB 2
Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443
                                                                                                                                                                                                                                                                                    .5; DB 2; Length 868; 2.8e-07; hes 173; Indels 101
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A;Cross-references: GDB:127545; OMIM:107266
A;Map position: 19q13.1-19q13.1
C;Superfamily: immunoglobulin homology
C;Reywords: alternative splicing; B-cell; cell adhesion;
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-510/Domain: extracellular #status predicted <EXT>F;432-484/Domain: immunoglobulin homology <IMM>F;511-529/Domain: transmembrane #status predicted <TMM>F;530-647/Domain: intracellular #status predicted <CYT>F;530-647/Domain: intracellular #status predicted <CYT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B-cell adhesion protein CD22 alpha splice form precursor - human C;Species: Homo sapiens (man) C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB: CD22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:x52785; NID:g29778; PIDN:CAA36988.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-647 < STA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: A35648
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A35648
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Best Local
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                285
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                                                                                                                                                                                                                                                                                                                                                                                                1 MLLPLLLSSLLGGSQAMDGRFWI-RVQESVMVPEGLCISVPCSFS------YPRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
           WEEPSLGVLKIQNVGWDNTTIACAACNSWCSWASPVALNVQYAPRDVRVRKIKPLSEIHS
                                                                                                                                                SCYGYPIQLQWLLEGVPMRQAAVTSTSLTIKSVFTRSELKFSPQWSHHGKI-VTCQLQDA
                                                                                                                                                                                                                       HLNDSGQLGLRMES----KTEKWMERIHLNVSERPFPPHIQLPPEIQESQEVTLTCLLNF 165
                                                                                                                                                                                                                                                        QMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFN- 167
                                                                                                                                                                                                                                                                                                                           DWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDA 108
                                                                                                                                                                                                                                                                                                                                                              LLGPWLLLLVLEYLAFSDSSKWVFEHPETLYAWEGACVWIPCTYRALDGDLESFILFHNP
                                                                                                                                                                                                                                                                                            EYNKNTSKFD--GTRLYESTKDGKVP-----SEQKRVQFLGDKNK-NCTLSIHPV
                                                                               DGKFLSNDTVQLNVKHPPKKVTTVIQNPMPIREGDTVTLSCNYNSSNPSVTRYEWKPHGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                       --WAFEECPPPSFSWTGAALSSQGT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.68;
19.08;
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MUID:90231465;
                                                                                                                                                                                                                                                                                                                                                                                                                                           87;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 206.5; DB 2;
Pred. No. 1.8e-06;
7; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monocyte and erythrocyte adhesion
; PMID:1691828
                                              SAQRTVRLRVAYAPRDL - - - -
                                                                                                                                                                                     -----KPTTSHFSVLSFTPRPQDH
                                                                                                                 TDLTCHVDFSRKGV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carbohydrate (Asn) (covalent)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     257;
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	QY 1 MLLPLLLSSLLGGSQAMDGRFWI-RVQESVMVPEGLCISVPCSFSYPRQ 48	
	Query Match 7.5%; Score 202.5; DB 2; Length 847; Best Local Similarity 21.0%; Pred. No. 4.7e-06; Matches 98; Conservative 69; Mismatches 182; Indels 117; Gaps 19;	
<u> </u>	F;609-661/Domain: immunoglobulin homology <imm2> F;688-706/Domain: transmembrane #status predicted <tra> F;688-706/Domain: transmembrane #status predicted <tra> F;67,101,112,135,164,231,363,445,448,479,574,634/Binding site: carbohydrate (Asn) (covair;764,789/Binding site: phosphate (Thr) (covalent) #status predicted</tra></tra></imm2>	
	C:Keywords: alternative splicing: B-cell; cell adhesion; dimer; glycoprotein; phosphoprote; 1-19/Domain: signal sequence #status predicted <sig> F; 20-847/Product: B lymphocyte cell adhesion protein #status predicted <mat> F; 346-398/Domain: immunoglobulin homology <immi></immi></mat></sig>	
	A:Coros: references: GDB:127545; OMIM:107266 A:Cross: references: GDB:127545; OMIM:107266 A:Map position: 19q13.1-19q13.1 A:Introns: 138/1; 240/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3 C:Suberfamily: immunoclobulin homology	
	A; Molecule type: DNA A; Molecule type: DNA A; Residues: 121-269,'T',271-473,'K',475-614,'R',616-638,'Y',640-711,777-847 <wilz> A; Cross-references: GB:S61375; NID:g385980; PIDN:AAC18956.1; PID:g3184492 C; Genetics: CB:CFC</wilz>	
	Title: Genomic stru Reference number: 1 Accession: I56171	
	358 as	
	A;Molecule type: mRNA A;Residues: 1-847 <will> A;Cross-references: GB:X59350; NID:g36090; PIDN:CAA42006.1; PID:g36091 A;Experimental source: B lymphocyte</will>	
	A;Title: CDNA clonding of the B cell membrane protein CD22: a mediator of B-B cell inter A;Reference number: JH0371; MUID:91086838; PMID:1985119 A;Accession: JH0371	
	C;Accession: JH0371; F5cquence_revision or sep_1331 *cext_change 31"oan"2000 C;Accession: JH0371; F5c171	
	recursor - human	
	RESULT 12	
	Qy 485 LNFPGVRPRPEARMPKGTQADYAEVK 510	
	Db 555 VRNKKVRRAPLSEG	
	QY 425 KRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQEELHYAT 484	
	QY 371 IGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQ 424	
	Db 459 SLPYHSQKLRLEPYKYQHSGAYWCQGTNSYGKGRSPLSTLTYYYSPETIGRRYA 512	
	QY 312 SQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLS-LSVHYKKGLISTAFSNGAFLG 370	
•	405 SKAWTLEVLYAPRRLRVSMSPGDQVMEGKSATLTCESDANPPVSHYTWFDWNNQ	
	GNGTSLPVLLSWTQRGQVLSP	
	345 GNSVSLQCDFSSSHPKEVQFFWEKNGRLLGKESQLNFDSISPEDAGSYSCWVNNSIGQTA	
_	Qy 242VISISRDNTPDPPENLRVMVSQANRTVLENL 272	

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SCVAENILGTGQRGPGAELDVQYPPKKVTTVIQNPMPIREGDTVTL
                              TCHARHPLGS--QHVSLSLSVHYKKGLISTAFSNGAFLGIGITALL 377
                                                                                                                                                                                                QDADGKFLSNDTVQLNVKHTPKLEIKVTPSDAIVREGDSVTMTCEVSSSN----PEYTTV
                                                                                                                                                                                                                                                                                                                                                           QMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFN- 167
                                                                                                                                                                                                                                                                                                                                                                                               EYNKNTSKFD--GTRLYESTKDGKVP----
                                                                ILHSPAVEGSQVEFLCMSLANPLPTNYTWYHNGKEM--
                                                                                                                                 SWLKDGTSLKKQNTFTLNLREVTKDQSGKYCCQVSNDVGPGRSEEVFLQVQYAPEPSTVQ
                                                                                                                                                                                                                                                                                                                              HLNDSGQLGLRMES - - - - KTEKWMERIHLNVSERPFPPHIQLPPEIQESQEVTLTCLLNF
                                                                                                                                                                                                                                                                                                                                                                                                                            DWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDA 108
                                                                                                                                                                                                                                                              SCYGYPIQLQWLLEGVPMRQAAVTSTSL----TIKSVFTRSELKFSPQWSHHGKIVTCQL 221
                                                                                                 ---LPVLEGQSLCLVCVTHSSP-PARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEF 333
                                                                                                                                                                                                                             -DFSRKGVS-----AQRTVRLRVAYAPRDLVI------SISRDNTPDPPE----
                                                                                                                                                                                                                                                                                           WAFEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHV 217
                                                                                                                                                                ·····NLR-VMVSQANR-·-TVLENLGNGTS-------
                                                                                                                                                                                                                                                                                                                                                                                             -SEQKRVQFLGDKNK-NCTLSIHPV 109
                                                                QGRTEEKVHIPKILPWHAGTY
 440
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RESULT 13
A32164
A32164
blilary glycoprotein 1 precursor, splice form a - human
blilary glycoprotein 1 precursor, splice form a - human
N;Alternate names: transmembrane carcinoembryonic antigen 1 (TM1-CEA); transmembrane
N;Contains: biliary glycoprotein 1, splice form b; biliary glycoprotein 1, splice for
C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000
C;Accession: A32164; A30127; B30127; A48078; S45664; S65939; A30847; G44476
R;Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Heft
Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989
A;Reference number: A32164 R;Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J. Cell Biol. 108, 267-276, 1989
A;Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mR A;Reference number: A92752; MUID:89139550; PMID:2537311
A;Accession: A30127 A; Molecule type: mRNA
A; Residues: 1-319, 'D', 417-526 <BAR2>
A; Cross-references: EMBL:X14831; NID:937199;
A; Experimental source: splice form b
R; Barnett, T.R.; Drake, L.; Pickle II, W.
Mol. Cell. Biol. 13, 1273-1282, 1993 A; Molecule type: mRNA A; Residues: 1-526 <BARl> A; Cross-references: EMBL A;Contents: annotation
A;Contents: annotation
A;Contents: annotation
A;Note: the sequence shown in this reference has been completely corrected in referen A;Cross-references: GB:J03858; NID:g179439; PIDN:AAA51826.1; PID:g179440
R;Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Heft
Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988
A;Title: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure
A;Reference number: A94206; MUID:88320555; PMID:2457922 A;Accession: A48078 A;Molecule type: mRNA A;Residues: 124-141,'H',417-526 <BAR3> A; Title: Human biliary glycoprotein gene: characterization A; Reference number: A48078; MUID:93140765; PMID:8423792 A; Reference number: A; Accession: A48078 A; Accession: A; Experimental source: splice A; Residues: A; Molecule type: mRNA A; Accession: A32164 A;Contents: erratum 1-526 <HIN> B30127 EMBL: X16354; NID: g37197; PIDN: CAA34404.1; PID: g37198; EMBL: X14784 form PIDN:CAA32940.1; of a family of novel alter PID: g37200; EMBL: X14784

-----TAGP 421

-PSPESKKN

467 451 409

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F;160-217/Domain: immunoglobulin nomology <1MM2>
F;252-301/Domain: immunoglobulin homology <1MM2>
F;252-301/Domain: immunoglobulin homology <1MM3>
F;341-388/Domain: immunoglobulin homology <1MM3>
F;442-345/Domain: transmembrane #status predicted <7MM>
F;425-454/Domain: intracellular #status predicted <INT>
F;453-526/Domain: intracellular #status predicted <INT>
F;104,111,115,152,182,197,208,224,232,254,274,288,292,302,309,345,351,363,378,405,475/Bi
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C; Superfamily: carcinoembryonic antigen; car
C; Keywords: alternative splicing.
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
A;Note: only a part of the coding sequence is given
R;Khan, W., Freengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S.
Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoembra.
A;Reference number: A44476; MUID:33052339; PMID:1427854
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A;Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; A;Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; R;Nedellec, P.; Turbide, C.; Beauchemin, N. Eur. J. Blochem. 231, 104-114, 1995
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A; Residues: 1-21 <NED>
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A; Note: neither the complete nucleic acid sequence nor the complete translation are R; Hauck, W; Nedellec, P.; Turbide, C.; Stanners, C.P.; Barnett, T.R.; Beauchemin, N Eur. J. Biochem. 223, 529-541, 1994
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Best Local S
Matches 130
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A;Experimental source: splice form x
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                    ----GQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHAR
                                                                                                                                   VRLRVAYAPRDL-VISISRDNTPDPPENLRVMVSQANRT--VLENLGNGTSLPVLE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GY-WFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKG-----NCSLVIRDAQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLLSSLLGGSQAMDGRFWIRVQESYMVPEGLCISVP-----CSFSYPRQDWTGSTPAY 57
                                                                                                                                                                                                                                              FEECPPPSFSWTGAALSSOGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT
                                                                                                                                                                                                                                                                                                               QNDTGFYTLQV-----IKSDLVNE----EATGQFHVY
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                                                                          -RLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVS-ANRSDPVTLNVTYGPDTPTISPSDT
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                                                                                                                                                                                              ---ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWWINNQSLPVSP---
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A;Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1;
C;Superfamily: advanced glycosylation end products
C;Keywords: receptor; transmembrane protein
E;31-100/Domain: immunoglobulin homology < TMM>
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C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
C:Accession: T09062
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A; Residues: 1-402 <R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mahairas, G.;
LGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQ
                                                                                                                       PRVQVEHEGEFTCHARHPLGSQHVSLSLSVHY--
                                                                                                                                                                                                                QANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLEL
                                                                                                                                                                                                                                                                                                                                             TPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPDPPENLRVMVS
                                                                                                                                                                                                                                                                                                                                                                                                      SVPNKVGTCVSEGSY---PAGTLSWHLDGKLLIPDGKETLVKEETRRHPETGLFTLRSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCSLVIRDAQMQDESQYFFRV--ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPET-LEP
                                                        PEVGHEDEGTYSCVATHPSHGPQESPPVSIRVTETGDEGPAEGSVGESGLGTLALALGIL
                                                                                                                                                                                        PEGGI--
                                                                                                                                                                                                                                                                                       TVIPTQGGTHPTFSCSFS-LGLPRRRPLNT----APIQL-----RVREPGPPEGIQLLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQPVTV-ICVFNWAFEECPPPSFSW--TGAALSSQGTK------PTTSHFSVLS-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGSLLLPATGIVDEGTFRCRATNRRGKEVKSNYR-----VRVYQIPGKPEIVDPASELTA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEVKKQ 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKKQYQLPSFPEPKSSTQ--APESQESQEELHYATLNFPGVRP-RPEARMPK--GTQADY 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEVKFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L----IIMKILPKRRTQTETPRPRFSRHSTILDYINVVP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPL-GSQHVSLSLSVHYKKGLISTAFS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL:AF030001; NID:g2564945; PID:g2564950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qln, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, Library, October 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the mouse major histocompatibility locus class III region
                                                                                                                                                                            -VAPGGTVTLTCAISAQPPPQVHWIKDGAPL-PLAPSP--VLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 184; DB
Pred. No. 3.4e
46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272/3; 320/1; 329/1; 371, receptor; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NGAFLGIGITALLFLCLA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 146;
                                                                                                                    -KKGLISTAFSNGAF
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Gaps

156

346 368 286 322 241 262 191 202 371/2 ulin homology

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A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD protein addression molecules, and epidermal growth factor.

A;Reference number: A41736; MUID:92112994; PMID:1730768
A;Reference number: S19256
A;Rolecule type: mRNA
A;Residues: 1-57, D, 59-434, 'A',436, 'FL',438-449, 'Q',451-502, 'A',503-792, 'K',794-908, 'R'
A;Cross references: EMBL:X65515
A;Cross references: EMBL:X65515
A;Reference number: S77966
A;Reference number: S77966
A;Reference number: S7996
A;Receasion: S77966
A;Receasion: S77966
A;Reference number: S7996
A;Receasion: S77967
A;Cross references: EMBL:X65515; NID:g2969; PIIN:CAA4373.1; PID:g24470
A;Cross references: EMBL:X65515; NID:g2969; PIIN:CAA4373.1; PID:g24370
A;Reference number: A41059
A;Reference number: A41059
A;Reference number: A41059
A;Reference number: A41059; MUID:92120660; PMID:1685141
A;Reference number: A41059; MUID:92120660; PMID:16851
      anes.

A; Reference number: A33625; MUID:90078352

A; Accession: B33625

A; Molecule type: protein
A; Residues: 1379-1384,'X',1386-1388,'X',13
A; Accession: A33625

A; Molecule type: protein
A; Residues: 2166-2171,'X',2173-2175,'X',2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 05-Nov-199
C:Accession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A4173
R:Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.
J. Biol. Chem. 267, 8544-8557, 1992
A:Title: Primary structure of the human heparan sulfate proteoglycan from tor, laminin, neural cell adhesion molecules, and epidermal growth factor.
A:Reference number: A38096; MUID:92233084; PMID:1569102
A:Accession: A38096; AUID:92233084; PMID:1569102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-4391 <MUR>
A; Residues: 1-4391 <MUR>
A; Cross-references: GB: M85289; NID:g184426;
R; Kallunki, P.; Tryggvason, K.
J. Cell Biol. 116, 559-571, 1992
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A38096
A38096
perlecan precursor - human
perlecan precursor - human
n;Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate
C;Specles: Homo sapiens (man)
C;Specles: Homo sapiens (man)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 05-Nov-1999
C;Accession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A41736
                                                                                                                                                                                                                                      R;Heremans, A.; van der Schueren, B.; De Cock, B.; Paulss
J. Cell Biol. 109, 3199-3211, 1989
A;Title: Matrix-associated heparan sulfate proteoglycan:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B & B
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;Molecule type: protein
;Residues: 2166-2171,'x',2173-2175,'x',2177-2185
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                                                                                                                                                                                        MUID:90078352;
                                                                                                                                                                                        PMID: 2687294
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                                                                                                                                                                                                                                                                                                       B.; Paulsson,
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M.; Cassiman,
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                                                                                                                                                                                                                                            protein-specific
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VGAILWRKRQ
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F;331-1676/Domain: Laminin-type EGF-like homology <LEG>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG>
F;153-1610/Domain: laminin-type EGF-like homology <LEGP>
F;163-1686/Domain: IV <DOM4>
F;1677-3686/Domain: IV <DOM4>
F;1677-3686/Domain: LCANSMEMBRANE #Status predicted <TRM>
F;2007-2034/Domain: LCANSMEMPRANE #Status predicted <TRM>
F;3845-3880/Domain: EGF homology <LGFP>
F;3845-3880/Domain: EGF homology <LGFP>
F;3845-3880/Domain: LAMINING Grepeat homology <LGFP>
F;3847-4175/Domain: EGF homology <LGFP>
F;4147-4175/Domain: EGF homology <LGFP>
F;4147-4175/Domain: EGF homology <LGFP>
F;4149-4151/Region: motor neuron attachment (L-R-E) motif E;4299-4301/Region: motor neuron attachment (L-R-E) motif E;65,71,76/Binding site: heparan sulfate (Ser) (covalent) #status predicted E;89,554,1755,2121,3072,3105,3279,3780,3836,4068/Binding site: carbohydrate (Asn E;89)-534,375,3193,34179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted predicted files for the constant of the covalent of the covalent
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F;12-193/Domain: II <DOM2>
F;194-530/Domain: II <DOM2>
F;199-334/Domain: LDL receptor ligand-binding F;285-319/Domain: LDL receptor ligand-binding F;285-319/Domain: LDL receptor ligand-binding F;325-359/Domain: LDL receptor ligand-binding F;325-359/Domain: LDL receptor ligand-binding F;325-359/Domain: LDL receptor ligand-binding F;325-359/Domain: LDL receptor ligand-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSLPGR--ATARNELLHFERAAPEDSGRYRCRV--TNKVGSAEAFAQLLVQGPPGSLPAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SISRDNTPDPPENLRYMVSQANRTVLENLGNGTSLPVLE - - - - GQSLCLVCVTHSSPPAR
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                                                                                                        GGVVRIAHVELADAGQYRCTATNAAGTTQSHVLLLVQALPQISMPQEVRVPAGSAAVFPC
                                                                                                                                                                                                                                                                                                                                                                                                                       STAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRWFKEGGQLPPGHSVQDGVLRIQNLDQSCQGTYICQAHGPWGKAQASAQLVIQALPSVL
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                                                                                                                                                                                                           ----RHSTILD----YINVVPTAGP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----FKAVTETTKGAPVATNHQSREVEMSTRG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -KGNCSLVIRDAQMQDESQYFFRVERGSYVRYNF
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                                                                                                                                                                                                           -LAQKRNQKATPNSPRTP---
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1 MLLPLLLSSLLGGS
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        SwissProt_41:*
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J. BIOÌ. Chem. [4] SEQUENCE FROM AND 5), MUTAGE MEDLINE-221528 Kitzig F., Mar "Cloning of tw interaction be Biochem. Bioph [5] SEQUENCE OF 33 TISSUE-B cell; MEDLINE-223882 Strausberg R.L Klausner R.D. Altschul S.F., Diatchenko L., Stapleton M.,	SEQUENCE FROM N.A. (ISOFORM 1 SEQUENCE FROM N.A. (ISOFORM 1 TISSUE-Spleen; MEDLINE-21181584; PubMed-1128 Munday J., Kerr S., Ni J., Moore Floyd H., Mattel MG., Moore "Identification, characteriza siglec-10, a novel human sial blochem. J. 353:489-497(2001) [3] SEQUENCE FROM N.A. (ISOFORM 2 TISSUE-Dendritic cell; MEDLINE-21359381; PubMed-2135 Li N., Zhang W., Wan T., Zhang and characterization binding member of the Ig super the state of the Ig state of the Ig super the state of the Ig stat	like protein 2). SIGLECIO OR SLG2. Homo sapiens (Huma Eukaryota; Metazoa Mammalia; Eutheria NCBL_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=21303047; Yousef G.M., Ordon "Molecular charact Siglec-like gene ( Biochem. Blophys.	AN A_HUMAN A_EB-20C FEB-20C SEP-20C SEP-20C	153.5 147.5 147.5 147.5 143.5 141.5 140.5 140.5 140.5 139.5 139.5 138.5
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276:28106-28112(2001 N.A. (ISOFORM 3), ALT SNESIS OF TYR-667, AND 900; PubMed=12163025; ttiner-Barricoanal A, yo new splice variants tween Siglec-10 and S stween Siglec-10 and S s s stween Siglec-10 and S s s s s s s s s s s s s s s s s s s s	M N.A. (ISOFORM 1).  n; 1184; PubMed=11284738; 1184; Ni J., Cornish ttei M. G., Moore P., ion, characterization novel human sialic ac 355:489-497(2001).  M N.A. (ISOFORM 2). ittc cell; 11358961; 9381; PubMed=11358961; 9381; PubMed=11358961; characterization of S characterization of S characterization of S	(ISO	TANDARD; 16G54; Q96LC8; 13 (Rel. 41, Create 13 (Rel. 41, Last s 13 (Rel. 42, Last a 13 d binding Ig·like	1241 1206 702 702 417 739 428 628 628 419 404
6-28112(200) FORM 3), AL: TYR-667, ANI dd-12163025; riocanal A. ice variant: lec-10 and i Commun. 296 Commun. 296 M N.A. (ISO) M N.A. (ISO) dd-12477932; ld E.A., Gro F.S., Wagne, B., Buetow , Moore T., , K., Farmer	SOFORM 1).  Legal 1284738  Legal 1284738  Legal 1284738  Legal 1284738  Moore P.  Moor	J 80	d) pnno nno	RAGE 1 NPHN 1 KMLS 1 CEAS 1 CEAS 1 PVR H 1 PVG1 1 PSG3 1 LU_HU 1 PSG7 1 RAGE 1 CEA8 1 CEA8
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RACTION WITH:  Botet M., S.  Glec-10 and:  S2(2002).  S3/4).  H., Derge J.  Shenmen C.M.,  Schaefer C.F.  I., Wang J.,  Rubin G.M.,  Casavant T.L	hang J.Q., Nic Crocker P.R.; ocyte expressi ng receptor. ", ocyte expressi ocyte expressi ocyte expressi ocyte expressi ng receptor. ",	Vertebrata; Hominidae amandis E.p erssion, and ersvion, and evariants:	or (Sigle	
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards J., Holton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Ra Hilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RRA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Proc. Natl. Assay Sequences.", "Generation and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

C. - FUNCTION: Putative adhesion molecule that mediates sialic-acid conception with stalic acid recognition site may be masked by cis interactions with stalic acids on the same cell surface. In the immune response, may act as an inhibitory receptor cytoplasmic phosphatase(s) via their SH2 domain(s) that block molecules.

C. molecules.
                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                          L; AY029277; AAK40255.1; -. AY029277; AAK40256.1; -. AY029277; AAK50256.1; -. AF310233; AAK55139.1; -. AF311955; AAK92542.1; -. AY032685; AAK91124.1; -. BC009955; AAH09955.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: Tyrosine-phosphorylated.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.

SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (eosinophils, monocytes and a natural killer cell subpopulation). Isoform 5 is found to be the most abundant isoform. Found in lymph node, lung, ovary and appendix. Isoform 1 is found at high levels and isoform 2 at lower levels in bone marrow, spleen and spinal chord. Isoform 2 is also found in brain. Isoform 4 is specifically found in natural killer cells.

DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular functions as the termination of the immune response. The phosphorylated ITIM motif pinds to the SH2 domain of PTPN6/SHP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Wyu-...
Name=3; Synonyms=Sv3;
IsoId=096LC7-3; Sequence=VSP_002564;
IsoId=096LC7-4; Sequence=VSP_002561;
IsoId=096LC7-4; Sequence=VSP_002562;
Name=5; Synonyms=Sv2;
IsoId=096LC7-5; Sequence=VSP_002562, VSP_002563;
IsoId=096LC7-5; Sequence=VSP_002561, VSP_002563;
IsoId=096LC7-6; Sequence=VSP_002561;
IsoId=096LC7-6; S
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ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=2; Synonyms=Short, Sv1;
IsoId=Q96LC7-2; Sequence=VSP_002565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
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IsoId=Q96LC7-1; Sequence=Displayed;
                                                    HGNC:15620; SIGLEC10.
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SMART; SM00409; IG; 4.
SMART; SM00409; IGc2; 2.
PROSITE; PS50835; IG_LIKE; 1
PROSITE; PS00290; IG_MHC; 1.
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       121
                                 121
                                                               61
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                                                                                                                                                                                                 Similarity
ERGSYVRYNEMNDGEFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
              ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                        FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                   MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                           FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                   MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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IPR003598;
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
ITH MOTIF 1.
ITH MOTIF 1.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
                                                                                                                                                                              Score 2576.5; DB 1
Pred. No. 1.8e-173;
1; Mismatches 2;
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P -> S
L -> P
R -> K
P -> S
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S -> P (IN REF. 4).
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V -> A (IN REF. 1).
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TGAAL -> TGMRWGGNPCLSHWGGTLGTAYGLSREGSQGP
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"Cloning and characterization of human Siglec-11. A recently evolved risignaling that can interact with SHP-1 and SHP-2 and is expressed by RT signaling that can interact with SHP-1 and SHP-2; and is expressed by RT tissue macrophages, including brain microglia.";
RT J Biol. Chem. 277:24466-24474(2002).

CC -i- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2,8-CC linked sialic acid. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface. In the immune response, may act as an inhibitory receptor upon ligand composition in the immune response, may act as an inhibitory receptor upon ligand induced tyrosine phosphorylation by recruiting cytoplasmic phosphatase(s) via their SH2 domain(s) that block signal transduction through dephosphorylation of signaling molecules. CC composition with prpN6/SHP-1 and prpN11/SHP-2 upon phosphorylation.

CC -i- SUBCHILULAR LOCATION: Type I membrane protein.

CC -i- TISSUE SPECIFICITY: Expressed by macrophages in various tissues
                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
51alic acid binding Ig-like lectin 11 precursor (Siglec-11) (Sialic acid-binding lectin 11).
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND INTERACTION WITH PTPN6 AND MEDLINE-22086217; PubMed-11986327; Angata T., Kerr S.C., Greaves D.R., Varki N.M., Cro
                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SILB_HUMAN
Q96RL6;
                                                                                                                                                                                                                                                                                                                                                                                 SIGLEC11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                     Chordata; Primates;
                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                  181
                                                122
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 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                              ERGSYVRYNEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                                                                                        FKAVTETTKGAPVATNHQSREVEMSTRGREQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                 ERGSRVRHSFLSNAFFLKVTALTKKPDVYIPETLEPGQPVTVICVFNWAFKKCPAPSFSW
                                                                                                          FKGRTSPKTGAPVATNNQSREVEMSTRDRFQLTGDPGKGSCSLVIRDAQREDEAWYFFRV
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Pfam; PF00047; 19; 3.
SMART; SM00408; IGC2; 2.
PROSITE; PS50835; IG_LIKE; 3
PROSITE; PS00290; IG_MHC; 1.
Cell adhesion; Lectin; Trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 607157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF337818; AAK72907.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: Phosphorylated on tyrosine residues.
SIMILARITY: Belongs to the immunoglobulin superfamily. SIGL
(SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          including Kupffer cells. Also found in brain microglia. DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This is involved in downmodulation of cellular functions as the termination of the immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:15622; SIGLEC11.
                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR007110;
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16
550
573
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lectin;
domain;
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Ig_MHC.
                         55.98;
46.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane; Signal; (Repeat; Phosphorylation
51;
                                                                                POTENTIAL:
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE 1.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
ITHM MOTIF
BY SIMILARITY.
BY S
  Score 1513.5;
Pred. No. 7.4e
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
SIALIC ACID BINDING IG-LII
EXTRACELLULAR (POTENTIAL)
                         5; DB
.4e-99;
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                                                                                         CRC64;
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  Indels
                                                                                                                              (POTENTIAL).
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(POTENTIAL).
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                                           Length
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  Gaps
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120 61

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SIIB_HUMAN STANDARD; PRT; 499
Q9NYZ4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence upda
15-SEP-2003 (Rel. 42, Last annotation up
Sialic acid binding Ig-like lectin 8 pre
(Sialoadhesin family member-2) (SAF-2).
SIGLEC8 OR SAF2.
                                                                                                                                                                                     Kikly K.K., Bochher B.S., Freeman S.D., Tan K.B., Gallagher K. D'Alessio K.J., Holmes S.D., Abrahamson J.A., Erickson-Miller Murdook P.R., Tachimoto H., Schleimer R.P., White J.R., "Identification of SAF-2, a novel siglec expressed on eosinophmast cells, and basophils.", Allergy Clin. Immunol. 105:1093-1100(2000).
                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM TISSUE=Eosinophil;
                                                      "Siglec-8. A novel
                                                                                                                          MEDLINE=20092847;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 3), MEDLINE-20314554; PubMed=10856141; Kikly K.K., Bochner B.S., Freeman
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE-20549027; PubMed=11095983;

Foussias G., Yousef G.M., Diamandis E.P.;

"Molecular characterization of a siglec8 variant containing cytoplasmic tyrosine-based motifs, and mapping of the siglec8 cytoplasmic ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                              Ni J., Cornish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -ELHYASLSFQGLRLWEPADQEAPSTTEYSEIK 660
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                                                                                                                 PubMed=10625619;
                                                  eosinophil~specific
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Catarrhini; Hominidae;
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                                                                                         Carter
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                                                1mmunoglobulin
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Pfam; PF00047; 19; 2.
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE; 2.
Cell adhesion; Lectin; Transm
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EMBL; AF223403;
EMBL; AF195092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 605639; ... Go: 0016021; C:integral to membrane; GO: GO:0005330; F:lectin; TAS. GO: GO:0004888; F:transmembrane receptor GO: GO:0007165; P:signal transduction;
                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                           TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: Expressed specifically on eosinophils.
-!- DOMAIN: Contains an intracytoplasmic mottif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This mot is involved in downmodulation of cellular functions as the termination of the immune response.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floyd H., Zhang J.Q., Crocker P.R.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Floyd H., Zhang J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dependent binding to cells. Preferentially binds to alpha2,3-linked sialic acid. Also binds to alpha2,6-linked sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface.

SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF310234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:10877; SIGLEC8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9NYZ4-2; Sequence=VSP_002559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9NYZ4-3; Sequence=VSP_002560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9NYZ4-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR007110; Ig-lik
IPR003598; Ig_c2.
IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chem.
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               Lectin;

1 domain;

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7 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275:861-866(2000).
                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Signal; Glycoprotein; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence=Displayed;
ITIN MOTIF.

SLAM-LIKE MOTIF.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

ALTHREDILLIGTLESGHSRNLTCSVPWACKQGTPPMISWI
                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
                                                                                                                                                                                                                                                                                                     EXTRACELLULAR POTENTIAL.
                                                                                                                                                                                                                                                                                                                                              SIALIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor acuction; TAS.
                                                                                                                                                                                                                                                                                                                                          BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity; TAS
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RESULT 3
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Floyd H., Ni Crocker P.R.;

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DT 28-FEB
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DE Silke m
GN SIGLEC
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RP SEQUEN
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Best Local :
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                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Slalic acid binding Ig-like lectin-like 1 precursor
like molecule 1) (Siglec-L1).
SIGLECL1 OR SLA
   "Cloning and molecular
new putative member of
Biochem. Biophys. Res.
                                                   TISSUE-Bone marrow;
MEDLINE-21303046; PubMed=11409877;
Foussias G., Taylor S.M., Yousef G
Foussias E.P.;
Diamandis E.P.;
                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                     Q96PQ1;
                                                                                                                                                                                                                                                                                                                                                    SILL_HUMAN
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                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                              Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      -----APSSGE-EGELHYATLSFHKVKPQDPQGQ--EATDSEYSEIK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPKSSTQAPESQESQEELHYATLNFPGVRPR-PEARMPKGTQADYAEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAVNSNPPARLSWTRGSLTLCPSRSSNPGLLELPRVHVRDEGEFTCRAQNAQGSQHISLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRLDVSY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRLRVAYAPRDLVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVHGYWFRAGDRPYQDAPVATNNPDREVQAETQGRFQLLGDIWSNDCSLSIRDARKRDKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MLLPLLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGDTGMEDAKAIRGSASQGPLTESWKD----GNPLKKPPPAV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHSTILDYINVV----PTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSLQNEGTGTSRPVSQVTLAAVGGAGATALAFLSFCIFIIV-----RSCRKKSARPAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSVHYKKGLISTAFSN---GAFLGIGITALLFL--CLALIIMKILPKRRTQTETPRPRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKQGTPPMISWIGASVSSPG--PTTARSSVLTLTPKPQDHGTSLTCQVTLPGTGVTTTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYFFRLERGSMKWSYKSQLNYKTKQLSVFVTALTHRPDILILGTLESGHSRNLTCSVPWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MLLLLLLPLLWGTKGMEGDRQYGDGYLLQVQELVTVQEGLCVHVPCSFSYPQDGWTDSD
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                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                         (ISOFORMS
                                                                                                                                                                             Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.0%;
42.1%;
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       characterization of two sp
the Siglec-3-like subgroup
Commun. 284:887-899(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥,
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GASVSSPGPTTARSSVLTLTPKPQDHGTSLTCQVTLPGTGV
TTTSTVBLDVSY -> D (in isoform 2).
/FTIG-VSP_002559.
GPLTESWKDGNPLKKPPPANAPSSGEEGELHYATLSFHKVK
PQDPQGGEATDSEYSEIKIHKRETAETQACLRNHNPSSKEV
RG -> VSDVGFSTPSIQPGHL (in isoform 3).
                                                                                                                         LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RG -> VSDVGFSTPSIQPGHL (in isoform /FTId=VSP_002560. 086EFF989B74123C CRC64;
                                                                                                                                                                             Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPWNLTMTVFQGDATASTALGNGSSLSVLEGQSLRLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                        G.M.,
                                                                                                                           AND
                                                                                                                                                                                                                                                                                                                                                    595
                                                                                                                           SHORT)
                                                                      Tropak M.B.,
                                                                                                                                                                                           Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
?.9e-59;
                                                                                                                                                                                                                                                                                                                                                    ξ
                                                                                                                                                                             Hominidae;
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                     splice variants
oup of Siglecs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 499;
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                                                                      Ordon M.H.,
                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                (Siglec
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        InterPro; IPR007110; Iq
InterPro; IPR003598; Iq
InterPro; IPR003006; Iq
Pfam; PF00047; iq; 4.
   DISULFID
DISULFID
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Dony, Synchyms=Suc.,

Name=Short; Synonyms=SuG-S;

IsoId=O96PO1-1; Sequence=D1splayed;

IsoId=O96PO1-2; Sequence=VSP_002566;

Intersine and intersine and adrenal gland, fettal brain and testis.

Intersine and bone marrow; it is lower expressed in thyroid, placenta, thymus, trachea, stomach, lung, adrenal gland, fettal brain and testis.

Intersine and bone marrow; it is lower expressed in thyroid, placenta, thymus, trachea, stomach, lung, adrenal gland, fettal brain and testis.

Intersine and bone marrow; it is lower expressed in thyroid, placenta, thymus, trachea, stomach, lung, adrenal gland, fettal brain and testis.

Intersine and bone marrow; it is lower expressed in thyroid, placenta, trachea, stomach, lung, adrenal gland, fettal brain and testis.

Intersine and bone marrow; it is lower expressed in thyroid, placenta, stomach, lung, adrenal gland, fettal brain and testis.

Intersine and bone marrow; it is lower expressed in thyroid, placenta, stomach, lung, adrenal gland, fettal brain and testis.

Intersine and bone marrow; it is lower expressed in thyroid, placenta, stomach, lung, adrenal gland, fettal brain and testis.

Intersine and testis.

Intersine and bone marrow; it is lower expressed in thyroid, placenta, stomach, lung, adrenal gland, fettal brain and testis.

Intersine and testis.

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Angata T., Varki N.M., Varki A.;
Angata T. varki N.M., Varki A.;
A second uniquely human mutation affecting sialic
J. Biol. Chem. 276:40282-40287(2001).
-1- FUNCTION: Putative adhesion molecule that media
                                                                                                                         SITE
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DOMAIN
                                                                                                                                                                                                           DOMAIN
DOMAIN
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                            Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein; Immunoglobulin domain; Repeat; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF282256; AAK71521.1; Genew; HGNC:15482; SIGLECL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2] SEQUENCE FROM N.A. (ISOFORM LONG).
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                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00408; IO PROSITE; PS50835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 606094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SURFACE.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. The sialic acid recognition site m be masked by cis interactions with sialic acids on the same ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name~Long; Synonyms-SLG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF277806;
AF277806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; AAK51233.1; -.
; AAK51234.1; -.
; AAK71521.1; -.
                                                                                                                                                                                                                                                                                                                                                                                  IGc2; 1.
                                                                                                                                                                                                                                                                                                                                                                   IG_LIKE; 3.
       Ig_c2.
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SIAM-LIKE MOTIF.
SIAM-LIKE MOTIF.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC
                                                                                                                                                      IG-LIKE V-TYPE 1.
IG-LIKE V-TYPE 2.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                              SIALIC
                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                               ACID BINDING IG-LIKE
     (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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     (POTENTIAL).
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                                                                                                                                                                                                                                                                                                 LECTIN-LIKE
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GN SIGLEC
OS PAN tr.
OC Eukary
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Q95LH0;
Q95EB-2003
28-FEB-2003
28-FEB-2003
15-SEP-2003
Sialic acid
                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9598;
       MEDLINE=21523976;
                 SEQUENCE FROM
                                                                              SIGLECL1.
                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sialic acid binding Ig-like lectin-like 1 pre-
like molecule 1) (Siglec-L1).
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VARSPLIC
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                                                                  troglodytes (Chimpanzee).
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                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                   GYEYSEINIP 594
                                                                                                                                                                                                                                                      PLAQKRNQKATPNSPRTPLPP--GAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQE 478
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      PubMed=11546777;
                                             Chordata;
Primates;
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                                         Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 909; DB 1; 1
Pred. No. 1.7e-56;
5; Mismatches 174;
                                                                                                                                                PRT;
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N-LINKED
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/FTId=VSP_002566.
P -> T (in dbSNP:20:
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NMKWNYKYDQLSVNV -> PLLWANEERDSGGWADPRFS
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SFSYPQNGWTASDPVHGYWFRAGDHVSRNIPVATNNPARAV
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D05662176274C5C3 CRC64;
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D (GLCNAC...
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SALATARA ARARA ARA
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Best Local S
Matches 212
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SEQUENCE
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*A second uniquely human mutation affecting sialic acid biology.";

J. Biol. Chem. 276:40282-40287(2001).

-i- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. The sialic acid recognition site masked by cis interactions with sialic acids on the same cel
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SUBCELLUTAR LOCATION: Type I membrane protein.

DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This makes involved in downmodulation of cellular functions as the termination of the immune response.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLE (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.

SIMILARITY: Contains 2 immunoglobulin-like V-type domains.

SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                   127
                                                                               199
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                                                                                                                                                                                                                                                                                                                                                 Similarity
RYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSWTGAALS
                                                            IPCDIPVATNTPSGKVQEDTQGRFLLLGDPQTNNCSLSIRDARKGDSGKYYFQVERGSR-
                                                                                               TTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYV
                                                                                                                                                                               LSVNVTASQDLLSRYRLEVPESVTVQEGLCVSVPCSVLYPHCNWTASSPVYGSWFKEGAD
                                                                                                                                                                                                               LSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTE 66
                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                 70;
                                                                                                                                                                                                                                                                                                           Score 909; DB
Pred. No. 1.7e
70; Mismatches
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CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE 1.
IG-LIKE V-TYPE 2.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
ITIM MOTIF.
SLAM-LIKE MOTIF.
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                                                                                                                                                                                                                                                                                                                                        DB 1;
.7e-56;
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                                                                                                                                                                                                                                                                                                              164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Length 597;
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                                           SIIS_MOUSE STANDARD; PRT; 467 AA. 091Y57; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) stalic acid binding Ig-like lectin 5 precursor (Myeloid inhibitory siglec) (MIS).
                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                    SEQUENCE FROM N.A., PHOSPHORYLATION, MUTAGENESIS OF TYR TYR-455, AND INTERACTION WITH PTPN6 AND PTPN11.
MEDLINE-21092875; Pubmed-11171044;
Yu Z., Maoui M., Wu L., Banville D., Shen S.H.;
"mSiglec-E, a novel mouse CD33-related siglec (sialic a immunoglobulin-like lectin) that recruits Src homology
                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
    <del>: :</del>
                                                                                                                                                        TYR-455, AND INTERACTION WITH PTPN6 AND STRAIN-C57BL/6; TISSUE-Bone marrow;
                                                                                                                                                                           SEQUENCE FROM N.A.,
                                                                                                                                                                                                             (SH2)-domain-containing protein tyrosine phosphatases
                                                                                                                                                                                                                                                                                    NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                        σ
molecules.
SUBUNIT: Homodimer; disulfide-linked. Interacts with PTPN6/SHP-1 and PTPN1/SHP-2 upon phosphorylation.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed by monocytic/myeloid lineage cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYK---KGLISTAF
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                                                                                                                                                                                           353:483-492(2001).
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AND PTPN11.
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; Murinae; Mus
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            EMBL; AF317298; AAG38598.1; -.
EMBL; AF339269; AAK49917.1; -.
MGD; MGI:1932475; Siglec5.
GO; GO:0004872; F:receptor activity; II
GO; GO:0005057; F:receptor signaling pa
GO; GO:0007155; P:cell adhesion; IDA.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003098; Ig_C2.
InterPro; IPR003006; Ig_MHC.
                  CONFLICT
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SMART; SM00408; IGC2; 1.
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                                                      MUTAGEN
                                                                        MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: Phosphorylated on tyrosine residues.

SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.

(SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.

SIMILARITY: Contains 1 immunoglobulin-like V-type domains.

SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at higher levels in
           455
2
24
102
102
234
467
                                                                       46
167
197
216
227
227
237
237
244
262
262
287
294
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354
375
375
21
152
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430
453
170
170
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domain;
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                   Y->F: R
                                                                                                                                                                                 PHOSPHORYLATION (PTPN6 AND PTPN11)
PHOSPHORYLATION (
                                                               PTPN11
                                                                                                                                                                                                                                                                                                      POTENTIAL.
                  (IN REF. 2)
(IN REF. 2)
(IN REF. 2)
                                                       REDUCES
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spleen, liver and heart. Found at lower

levels in kidney and lung.

DOMAIN: Contains an intracytoplasmic motif referred as immunor-eceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular functions as the termination of the immune response. The phosphorylated ITIM motif binds to the SH2 domain of PTPN6/SHP-1 and PTPN11/SHP-2.

s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way non-profit institutions as long as its content is and this statement is not removed. Usage by and for requires a license agreement (See http://www.isb-sib. for .ch/announce/ commercia!

IDA. | protein activity;

Transmembrane; Signal; Glycoprotein; Repeat; Phosphorylation. SIALIC ACID BINDING IG-LIKE LECTIN EXTRACELLULAR (POTENTIAL). 5

ITIM MOTIF.
SLAM-LIKE MOTIF.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY. IG-LIKE V-TYPE.
IG-LIKE C2-TYPE
IG-LIKE C2-TYPE CYTOPLASMIC (POTENTIAL). (INVOLVED IN 1) (PROBABLE). 2 -BINDING Ö

PTPN6) (PROBABLE). N-LINKED (GLCNAC. (INVOLVED (POTENTIAL) (POTENTIAL) (POTENTIAL) IN BINDING ö

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N-LINKED (GLCNAC WKED (GLCNAC. WKED (GLCNAC. ABOLISHES BI BINDING BINDING ö (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL). Ö (POTENTIAL) PTPN6

54FD3E98950D2DEE CRC64;

Local Similarity

32.3%;

Score 873; DB 1; Pred. No. 4.2e-54;

Length 467;

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Db
Db
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                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=20357333; PubMed=10801862;

Zhang J.Q., Nicoll G., Jones C., Crocker F.

Zhang J.Q., Nicoll G., Jones C., Crocker F.

Siglec-9, a novel sialic acid binding men superfamily expressed broadly on human bl.

T. Biol. Chem. 275:22121-22126(2000).
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SEQUENCE /
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sialic acid-binding Ig-like lectin 9 precursor
TISSUE-Peripheral
            SEQUENCE FROM N.A.
                                                                                                                       Genom.
                                                                                                                            "Toussias G., Yousef G.M., Diamandis E.P.,
"Identification and molecular characterization
the siglec family (SIGLEC9).";
                                                                                                                                                                TISSUE-Bone marrow;
MEDLINE=20366134; PubMed=10903842;
                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                     67:171-178(2000).
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  blood
           AND MUTAGENESIS OF
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                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                   Crocker P.R.;
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Burkhart-Schultz K., Gordon L. Dias J., Ramirez M., Stilwagen S.,
A Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
A Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
A Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
A Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
A Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
A Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
A Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
A Olsen A.S., Carrano A.V.,
A Olsen A.S., Carrano A.V.,
A Olsen A.S., Carrano A.V.,
A Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
C "Sequence analysis of chromosome 19q13.4.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
C "IPUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2,3- or 2,6-linked sialic acid. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell
                                                   GO; GO:0007166; P:cell surface InterPro; IPR007110; Ig-like. InterPro; IPR003599; Ig. InterPro; IPR003599; Ig. MHC. Pfam; PF00047; Ig; 3.

SMART; SM00409; IG; 2.

PROSITE; PS50835; IG_LIKE; 3.
Cell adhesion; Lectin; Antigen; Transmembrane; Immunoglobulin domain; Repeat; Polymorphism. SIGNAL 1 17 POTENTIAL.
                                                                                                                                                                                                                                                                          EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                        Genew;
                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Lamerdin J.E., McC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              new member of the CD33-related group of co-evolution with sialic acid synthesis J. Biol. Chem. 275;22127-22135(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takayama K., Fujii Y., Turitani K.,
Amemiya C., Yajima Y., Yazaki M.;
"Molecular cloning of a novel gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angata T., Varki A.; "Cloning, characterization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20357334;
                                                                                                                                                                         GO:0005887;
GO:0005530;
GO:0007166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         brain, mammary, adrenal gland, colon, trachea, cerebellum, small intestine and spinal cordon.

DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This is involved in downmodulation of cellular functions as the termination of the immune response.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLI (STALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.

SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SURFACE.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed by peripheral blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (neutrophils and monocytes but not eosinophils). Found in liver, fetal liver, bone marrow, placenta, spleen and in lower levels in skeletel muscle, fetal brain, stomach, lung, thymus, prostate,
                                                                                                                                                                                                                                       605640;
                                                                                                                                                                                                                                                  ; AF247180; AAF
; AF227924; AAF
; AB026265; BAB;
; AC011473; AAG;
; AC011473; AAG;
                                                                                                                                                                                                                                                                                                                                                  AF135027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           r cloning of a novel gene, FOAP-9, whether in human macrophages.";
(APR-1999) to the EMBL/GenBank/DDBJ
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म
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                                                                                                                                                                         F:lectin; NAS.
P:cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McCready P.M.,
                                                                                                                                                                                                               C:integral
                                                                                                                                                                                                                                                      SIGLEC9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10801860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND VARIANT GLU-315.
Y., Turitani K., Naitou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and phylogenetic analysis of siglec-9, ted group of siglecs. Evidence for id synthesis pathways.";
                                                                                                                                                                                                             plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skowronski E., Viswanathan
, Dias J., Ramirez M., Stil
                                                                                                                                                                         receptor
                                                                                                                                                                                                           membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOAP-9, which are
                                                                                                                                                                         linked
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                                     Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerebellum, testis,
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                               Glycoprotein;
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MUTAGEN
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CARBOHYD
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                                                                                                                                                                                                                  SQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510 : || || :| :| :| :| :| :| :|
                                                                                                                                                               VISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVC---VTHSSPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTSVSP--LDPSTTRSSVLTLIPQPQDHGTSLTCQVTEPGASVTTNKTVHLNVSY----
                                                                                                                                                                                                                                                                                                                                                                                                                     GAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGSYVRYNFMNDGFFLKVTALTOKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLSSLLGGSQAMDGRF - - WIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTP - AYGYWF
                                                                SASQGPLTEPWAEDS------PPDQPPPASAR
                                                                                                                                          ATSGVTQGVVGGAGATALVFLSFCVIFVVV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGS-IKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSVPWACEQGTPPMISWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIYPGPVVHGYWF
                                                                                                   -PTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQE 475
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463
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CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE 1.

IG-LIKE C2-TYPE 2.

ITH MOTIF.

SLAM-LIKE MOTIF.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R->K: LOSS OF SIALIC ACID BINDING R -> H (IN REF. 2).
; 807BDCE0D18191F2 CRC64;
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N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 870; DB 1; Pred. No. 6.7e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId-VAR_014255
N -> K (in dbSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId-VAR_014257.
A -> D (in dbSNP:273688).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIALIC ACID-BINDING IG-LIKE LECTIN EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VAR_014254
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                                                                                                                                          RSCRKKSARPAAGVGDTGIEDANAVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                VSS
                                                              426
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RESULT 8

SIL6_HUMAN

ID LS_HUMAN

ID LS_HUMAN

ID LS_HUMAN

ID LS_HEEB

DT 28-FEB

DT 15-SEP

SIGLEC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C., Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F., Varki A., Kastelein R.A.;
J. Biol. Chem. 274:28058-28058(1999).

-I- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Binds to alpha2,6-linked sialic acid. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface.

-I- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04369; 015388; 043700;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Stalic acid binding Ig-like lectin 6 precursor
binding protein 1) (OB-BP1) (CD33 antigen-like
SIGLEC6 OR CD33L OR CD33L1 OR OBBP1.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "OB-BP1/Siglec-6. A leptin- and sialic immunoglobulin superfamily.";
J. Biol. Chem. 274:22729-22738(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patel N., Brinkman-Van der Linden
Balasubramanian S., Timans J.C., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Erythroleukemia; MEDLINE-99357812; PubMed-10428856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98127055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Varki A., Kastelein R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takei Y., Sasaki S., Fujiwara T., Takahashi E., Muto T., Nakamura Y.;
"Molecular cloning of a novel gene similar to myeloid antigen CD33 an
its specific expression in placenta.";
Cytogenet. Cell Genet. 78:295-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIL6_HUMAN
                                                                                                                                                      TISSUE SPECIFICITY: Expressed at high levels in placenta and syncytictrophoblastic cells) and at lower levels in speripheral blood leukocytes (predominantly B-cells) and sintestine.

DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (TINM). This involved in downmodulation of cellular functions as the termination of the immune response.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SI
                                                                              (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named iso Name=1; Synonyms=Membrane-bound, CD33 IsoId=043699-1; Sequence=Displayed; Name=2; Synonyms=Secreted, CD33L2; IsoId=043699-2; Sequence=VSP_002553 Note=Should not be confused with SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secreted (isoform 2).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             427 GEGELQYASLSFQMVKPW-DSRGQEATDTEYSEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=9465907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISOFORM 1), AND INTERACTION WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2).
                                                                                                                                                                                                                                                                                                                                                           sequence=VSP_002553, VSP_002554;
be confused with SIGLEC5 which has been called
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Peterson
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CD33L1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          isoforms-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Siglec-6) (Obesity-
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PROSITE; PS00290; IG_MHC; 1.
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SMART; SM00408; IGC2; 1.
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005887; C:integral to plasma membrane; GO; GO:0005624; C:membrane fraction; TAS. GO; GO:0007267; P:cell-cell signaling; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D86358; BAA24983.1; -. EMBL; U71382; AAB70702.1; -.
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entities
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                                                                                      N
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FRL-KSKWMKYGYTSSKLSVRVMALTHRPNISIPGTLESGHPSNLTCSVPWVCEQGTPPI
               FRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPS
                                                                             WFKAVTETTKGA--PVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYF
                                                                  MLPLLLPLLWAGALAQERRFQLEGPESLTVQEGLCVLVPCRLPTTLP-----ASYYGYGY
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                                ---LEGADVPVATNDPDEEVQEETRGRFHLLWDPRRKNCSLSIRDARRRDNAAYF
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BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 1
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RP -> A (IN REF. 2).
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N-LINKED
N-LINKED
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IG-LIKE C2-TYPE:
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                                                                                                                                                                       /FTId=VAR_014253.
LS -> IY (IN REF.
                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
KPEGRAGGVLGAVWGASITTLVFLCVCFIFRVKTRRKKAAQ
                                                                                                                                                                                        /FTId=VAR_014252
L -> F (in dbSNP)
                                                                                                                                                                                                               /FTId=VSP_002554
                                                                                                                                                                                                                                               PVQNTDDVNPVM ->
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                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                               FTId=VSP_002553.
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                                                                                                                                                                                                                                                                     (GLCNAC. .
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IN REF. 2).
> PGVWPS (IN REF. 7)
REF. 2).
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Angata T., Varki A.;
"Siglec-7: a sialic acid-binding lectin superfamily.";
Glycobiology 10:431-438(2000).
                                                      SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=20230158; PubMed=10764831;
                                                                                                  Zhang W., Wan T., Cao X.; "Characterization of a novel Submitted (AUG-1999) to the
                                                                                                                                                                                 Falco M., Blassoni R., Bottino C., Vitale M., Sivori S., Augugliaro R., Moretta L., Moretta A.;
"Identification and molecular cloning of p75/AIRM1, a novel member of the sialoadhesin family that functions as an inhibitory receptor in human natural killer cells.";
J. Exp. Med. 190:793-802(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _HUMAN
                                                                                                                                             TISSUE-Dendritic cell;
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Nicoll G., Ni J., Liu D., Klenerman P
Mattel M.-G., Crocker P.R.;
"Identification and characterization
expressed by human natural killer cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sialic acid binding Ig-like lectin 7 precursor membrane protein) (Adhesion inhibitory recptor (p75) (D-siglec)
SIGLECT OR AIRM1.
                                                                                                                                                                                                                                                                        TISSUE-Lymphoid;
MEDLINE=99429884; PubMed=10499918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).

Homo sapiens (Human).

Finkarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Q9Y286; Q9NZQ1; Q9UJ86; Q9UJ87; Q9Y502;
                                                                                                                                                                                                                                                                                                        INTERACTION WITH PTPN6
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20036547; PubMed=10567377;
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                                                                                                                                                            (ISOFORM
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dependent binding to cells. Preferentially binds to alpha2, 3 and alpha2,6-linked sialic acid. Also binds distalogangliosides (distalogalactosyl globoside, distalyl lactotetraosylceramide and distalyl GalNAc lactotetraosylceramide). The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface. In the immune response, may act as an inhibitory receptor upon ligand induced tyrosine phosphorylation by recruiting cytoplasmic phosphatase(s) via their SH2 domain(s) that block signal transduction through dephosphorylation of signaling molecules. Mediates inhibition of fignaling molecules. Mediates inhibits differentiation of CD34+ cell precursors towards myelomonocytic cell lineage and proliferation of leukemic myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vitale C., Romagnani C., Falco M., Ponte M., Vitale M., More Bacigalupo A., Moretta L., Mingari M.C.; "Engagement of p75/AIRM1 or CD33 inhibits the proliferation or leukemic myeloid cells.";
                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entitles requires a license agreement (See http://www.isbor send an email to license@isb-sib.ch).
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Ito A., Handa K., Withers D.A., Satch M., Hakomori S.;
"Binding specificity of siglec? to disialogangliosides of renal cell carcinoma: possible role of disialogangliosides in tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    progression
FEBS Lett. '
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                                                                                                                                                                                                                                       PTM: Tyrosine-phosphorylated.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.

SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

CAUTION: Ref. 3 sequence differs from that shown due to a frameshift in position 406.
                                                                                                                                                                                                                                                                                                                                                                                                Note=No experimental confirmation available;
TISSUE SPECIFICITY: Predominantly expressed by resting and activated natural killer cells and at lower levels by granulocytes and monocytes. High expression found in placenta, liver, lung, spleen, and peripheral blood leukocytes.

Spleen, and peripheral blood leukocytes.

DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular functions as the termination of the immune response. The phosphorylated ITIM motif binds to the SH2 domain of PTPN6/SHP-1.
                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Interacts with PTPN6/SHP-1 upon phosphorylation SUBCELLULAR LOCATION: Type I membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=4; Name=1; Synonyms=AIRM-1b;
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  AF170485;
AJ007395;
AJ130710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ame=2; Synonyms=AIRM-2;
IsoId=09Y286-2; Sequence=VSP_002555;
ame=3; Synonyms=AIRM-3;
IsoId=09Y286-3; Sequence=VSP_002556, VSP_002558;
Note=No experimental confirmation available;
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AAF12759.1; -. CAB46011.1; -. CAB51126.1; -.
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SMART; SM00408; IGc2; 1.
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
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                   180
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AJ130712;
AJ130713;
 236
                                                                                     Similarity
YAPRDLVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSS
                                                               YFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPP
                                                                                                                        MLLLLLPLLWGRERVEGQKSNRKDYSLTMQSSVTVQEGMCVHVRCSFSYPVDSQTDSDP
                                                                                                                                         LLPLLLSSLLGGSQAMDGR-----FWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTP
                  PMISWMGTSVSP--LHPSTTRSSVLTLIPQPQHHGTSLTCQVTLPGAGVTTNRTIQLNVS
                           PSFSWTGAALSSQGTKPTTSHESVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVA
                                                    YFFRMEKGN-IKWNYKYDQLSVNVTALTHRPNILIPGTLESGCFQNLTCSVPWACEQGTP
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51142
                                                                                                                                                                   30.8%; Score 832.5; DB 37.9%; Pred. No. 2.9e-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat;
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BY SIMILA
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N-LINKED
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V -> A (IN REF. 4).
8AFE44462B001F52 CRC64;
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GTSVSPLHPSTTRSSVLTLIPQPQHHGTSLTCQVTLPGAGV
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POTENTIAL.
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                                                                                                                                                                                                                                       -> G (in isoform 4).
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SIMILARITY.
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cis interactions

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id recognition site may acids on the same cell

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Arellano A., Sanders C., UW D., NOTH.
Olsen A.S., Carrano A.V.;
"Sequence analysis of a 5-Mb region in 19q13.4.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Putative adhesion molecule that mediates s
                                                                                 Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V., Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S., Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Erythroleukemia;
MEDLINE=99357812; pubMed=10428856;
Patel N. Brinkman-Van der Linden E.C.M.,
Balasubramanian S., Timans J.C., Peterson
Varki A., Kastelein R.A.;
                                                                                                                                                                                                                                                       Balasubramanian S., Timans
Varki A., Kastelein R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cornish A.L., Freeman S., Forbes G., Ni J., Zhang M., Cepeda M., Gentz R., Augustus M., Carter K.C., Crocker p.R.; "Characterization of siglec-5, a novel glycoprotein expressed on myeloid cells related to CD33."; Blood 92:2123-2132(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Stalic acid binding Ig-like lectin 5 precursor (Siglec-5) (Obesity-binding protein 2) (OB binding protein 2) (OB-BP2) (CD33 antigen-like 2) (CD170 antigen).
SIGLEC5 OR OBBP2 OR CD33L2.
                                                                                                                                                                                                                                                                                                                             "OB-BP1/Siglec-6. A leptin-and sialic acid-binding immunoglobulin superfamily."; J. Biol. Chem. 274:22729-22738(1999).
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Eukaryota; Metazoa; C
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                                                                                                                                                                                                                                      274:28058-28058(1999).
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Peterson
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D., Bell M.P., Bazan
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                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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InterPro; IPR003598;
InterPro; IPR003006;
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DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This involved in downmodulation of cellular functions as the termination of the immune response.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SI (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.

SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.
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TISSUE SPECIFICITY: Expressed by monocytic/myeloid lineage cells.
Found at high levels in peripheral blood leukocytes, spleen, bone marrow and at lower levels in lymph node, lung, appendix, placenta, pancreas and thymus. Expressed by monocytes and neutrophils but absent from leukemic cell lines representing earl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         surface.
SUBCELLULAR LOCATION:
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Ig_c2.
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Repeat; Antigen; Polymorphism
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/FTId=VAR_014251.
E -> K (IN REF. 1
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IG-LIKE C2-TYPE 1.
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SLAM-LIKE MOTIF.
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F -> S (in dbSNP
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Patel N., (3)

SEQUENCE

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CD33_HUMAN

P20138; OBTD24;

T 01-FEB-1991 (Rel. 17, Created)
T 01-FEB-1991 (Rel. 17, Last sequence update)
T 15-SEP-2003 (Rel. 42, Last annotation update)

""-aloid cell surface antigen CD33 precursor (
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Simmons D., Seed B.;
"Isolation of a cDNA encoding CD33,
myeloid progenitor cells.";
J. Immunol. 141:2797-2800(1988).
[2]
                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                        Homo sapiens (Human).
Homo sapiens (Human).
'--rvota; Metazoa; Chordata;
---heria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                TISSUE-Promonocytic lymphoma; MEDLINE-89009814; PubMed-3139766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPL-PPGAPS
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Pred. No. 3.3e
70; Mismatches
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Catarrhini; Hominidae;
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                                                                       differentiation
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Ra Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopkins R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Ra Haley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Ra Haley J., Hale S., Garcia A.M., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Green E.D., Dickson M.C., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", 17 June 15,000 full-length proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                     Vitale C., Romagnani C., Puccetti A., Olive D., Costello R., Chiossone L., Pitto A., Bacigalupo A., Moretta L., Mingari M.C.; "Surface expression and function of p75/AIRM-1 or CD33 in acute myeloid leukemias: engagement of CD33 induces apoptosis of leukem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTPN11, AND MUTAGENESIS OF TYR-340 MEDLINE=99223460; PubMed=10206955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYR-358, AND INTERACTION WITH MEDLINE-20025980; PubMed-10556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Freeman S.D., Keim S., Barber E.K., "Characterization of CD33 as a new of cellular interaction molecules." Blood 85:2005-2012(1995).
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           <u>.</u>
                                                                                                                                                                                                                                                                        cells.
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21244678; PubMed=11320212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taylor V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION OF TYR-340 AND TYR-358, PTPN11, AND MUTAGENESIS OF TYR-340.
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riverious Putative adhesion molecule of myslomonocytic-derived cells that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2,6-linked sialic acid. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface. In the immune response, mact as an inhibitory receptor upon ligand induced tyrosine phosphorylation by recruiting cytoplasmic phosphatase(s) via the SH2 domain(s) that block signal transduction through dephosphorylation of signaling molecules. Induces apoptosis in acute myeloid leukemia (in vitro).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myeloid-specific sialic acid-binding receithe protein-tyrosine phosphatases, SHP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-tyrosine phosphatases, Chem. 274:11505-11512(1999).
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Z
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                                                                                                                                                                                                                                                                                        induces apoptosis of leukemic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERACTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor, CD33, HP-1 and SHP-2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.R.;
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R MIM; 159590; -.

R GO; GO:0005887; C:integral to plasma membrane; TAS.

R GO; GO:0004872; F:receptor activity; TAS.

R GO; GO:0007267; F:cell-cell signaling; TAS.

R GO; GO:0007267; F:negative regulation of cell proliferation; TAS.

R GO; GO:0007165; F:negative regulation of cell proliferation; TAS.

R GO; GO:0007165; F:negative regulation of cell proliferation; TAS.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003599; Ig.

R InterPro; IPR003006; Ig_MHC.

R Pfam; PF00047; Ig; 2.

R PMCSITE; PS50835; IG_LIKE; 2.
      Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphorylation.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Monocytic/myeloid lineage cells.
-!- DOMAIN: Contains two copies of an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular functions as the binds to the SH2 domain of PTPNG/SHP-1 and/or PTPNIL/SHP-2.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBERMAILY.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-!- DATABASE: NAME=PROW; NOTE=CD guide CD33 entry:
-- WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd33.htm".
                                          MUTAGEN
CONFLICT
                                                                                                       CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                     DISULFID DISULFID DISULFID
                                 SEQUENCE
                                                                                            MUTAGEN
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                                                                                                                                                                                 MOD_RES
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DOMAIN
                                                                                                                                                                                                        MOD_RES
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EMBL; BC028152; AAH28152.1;
PIR; A30521; A30521.
HSSP; Q62230; 1QFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                          TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew;
       Match
                                                                                                                                                                                                                                                                                                                                                              adhesion; Lectin; Antigen; Transmembrane; Signal; Glycoprotein; phorylation; Immunoglobulin domain; Repeat; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M23197; AAA51948.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262230; 1QFO.
HGNC:1659; CD33.
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                              AA;
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                                                                                          100
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340
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     25.6%;
                              MW.
                                                                                                                                                                                                                        POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE.

IG-LIKE C2-TYPE.

ITIM MOTIF 1.

ITIM MOTIF 2.

BY SIMILARITY.

BY SIMILARITY.
                                                                                   N-LINKED (GLCNAC...) (P
Y->A: ABOLISHES BINDING T
                                                                 PTPN11;
CELLS.
                                       Y->A,F: REDUCES BINDING G -> R (IN REF. 2).
   Score 694;
                                                                                                                                                                                        PHOSPHORYLATION (INVOLVED IN PTPN6 AND PTPN11).
                                                                                                                                                                             PHOSPHORYLATION
                                                                                                                                                                   PTPN6
                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                          1973E196940FB16F
                                                                           INCREASES
                                                                                                                                                                                                                                                                                                                                          CELL SURFACE ANTIGEN CD33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
  DВ
                                                                                                                                                                           (INVOLVED IN BINDING
                                                                          BINDING OF
                          CRC64;
Length 364;
                                                                                                                          (POTENTIAL).
                                                                                                  (POTENTIAL)
                                                                                                                (POTENTIAL)
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                                                                                      TO PTPN6
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                                                                                                                                                                                                    BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         commercia
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RESULT 12
SILF_MOUSE
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gene clusters.;

J. Biol. Chem. 276:45128-45136(2001).

-!- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2,3-linked sialic acid. The sialic acid recognition site may be masked by cli interactions with sialic acids on the same cell surface.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Predominantly expressed by immature monocytic/myeloid lineage cells in both matrow. Also found at lower levels in mature neutrophils and monocytes.
-!- DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular functions as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                MEDLINE-2157625; PubMed-11579105;
MEDLINE-2157625; PubMed-11579105;
Angata T., Hingorani R., Varki N.M., Varki A.;
"Cloning and characterization of a novel mouse Siglec, mSiglec-F:
"Cloning and characterization of the mouse and human (CD33) Siglec-3-related
                                                                                                                                                                                                           gene clusters."
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEB-2003 (Rel. 42, Last annotation update)
Sialic acid binding Ig-like lectin-F precurso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SILF_MOUSE 0920G3;
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                         SIGLECF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYASLNFHGMNP-----SKDTSTEYSEVRTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYATLNFPGVRPRPEARMPKGTQADYAEVKFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLACKRNOKATPNSPRTPLPPGAPSPESKKNOKKQYQLPSFPEPKSSTQAPESQESQEEL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAXAPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----HGAIGGAGVTALLALCLCLIFFIVKTHRRKAARTAVGRNDTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERGSYVRYNEMNDGFFLKVTALTOKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSAAPTSLG--PRTTHSSVLIITPRPQDHGTNLTCQVKFAGAGVTTERTIQLNVTYVPQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FREGALISGDSPVATNKLDQEVQEETQGRFRLLGDPSRNNCSLSIVDARRRDNGSYFFRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQVFFRV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPLLLLLPLLWAGALAMDPNFWLQVQESVTVQEGLCVLVPCTFFHPIPYYDKNSPVHGYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGKQETRAGVV-----
                                                                                                                                                                                                                                                                                                                                                      Rodentia;
                                                                                                                                                                                                                                                                                                                                                                    Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.8%;
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                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleosto
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.1e-41;
9; Mismatches 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                   precursor
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                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-11ke.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; 1g; 2.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID DISULFID
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell adhesion; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF293371; AAL11043.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [mmunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               termination of the immune response.

SIMILARITY: Belongs to the immunoglobulin superfamily. SIGI (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.

SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                 302
                                                                 229
                                                                                                                                                        182
                                                                                                                                                                                     117
                                                                                                                                                                                                                   122
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                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                         LLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWF
                                                                                                                                        RGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSWT 181
                                                                                                                                                                                                                                                                   KAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVE 121
                                                                                                                                                                                                                                                                                                        LLPLLWA----GCLATDG-YSLSVTGSVTVQEGLCVFVACQVQYP----NSKGPVFGYWF
   WERPTQ--KPFQLSTPAELQLPRAELEDQGKYICQAQNSQGAQTASVSLSIRSLLQLLGP
                               WTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV-----
                                                                                          VISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLS
                                                                                                                                                                                                                                              REGANIFSGSPVATNDPQRSVLKEAQGRFYLMGKENSHNCSLDIRDAQKIDTGTYFFRLD
                                                                                                                        SSALTSLGHRTTLS--SELNLTPRPQDNGTNLTCQVNLPGTGVTVERTQQLSVIYA----
                                                                                                                                                                                     -GS-VKYSFQKSMLSVLVIALTEVPNIQVTSTLVSGNSTKLLCSVPWACEQGTPPIFSWM
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                  25.5%;
                                                              PQKMTIRVSWGDDTGTKVLQSGASLQIQEGESLSLVCMADSNPPAVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                      79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1
IG-LIKE C2-TYPE 2
ITIM MOTIF.
SLAM-LIKE MOTIF.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
Y SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
SIALIC ACID BINDING IG-LII
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                 Score 689.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                 8093838090484FC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C2-TYPE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE LECTIN-F
                                                                                                                                                                                                                                                                                                                                                                    Indels 173;
                                                                                                                                                                                                                                                                                                                                                                                              Length 569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _MOUSE
CD33_MOU
Q63994;
                                                                                                                                                       the
                                                                                                                        modified
                                                                                                                                                                                                                                  <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                           Name=33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            455
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                 IPR007110;
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STRAIN-BALB/C; TISSUE-Bone marrow; MEDLINE-94250900; PubMed-8193354; Tchilian E.Z., Beverley P.C., Young B.D., "Molecular cloning of two isoforms of the myeloid CD33 antigen."; Blood 83:3188-3198(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            063994; Q63997;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Myeloid cell surface antigen CD33 precursor (Siglec-3).
EMBL; S71345; AAB30842.1;
EMBL; S71403; AAB30843.2;
MGD; MGI:99440; Cd33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 33-A AND
                                                                                                                                                                                                                                                                                                                    IsoId-Q63994-2; Sequence-VSP_002534;
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC
(SIALIC ACID BINDING IG-LIKE LECTIN) SUBEAMILY.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                    European Bioinformatics Institute. The by non-profit institutions as long a lifted and this statement is not removed. It is requires a license agreement (See I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Putative adhesion molecule of myelomonocytic-derived cells that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2,6-linked sialic acid (By similarity). The sialic acid recognition site may be masked by interactions with sialic acids on the same cell surface. SUBCELLULAR LOCATION: Type I membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event-Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q63994-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PMP-PKPQNTEAMKSVYTEIK 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LALII---MKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRPRPEARMPKGTQADYAEVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splicing; Named isoforms=2;
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                                                                                                                                                                                               There are no restrictions ng as its content is in
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                                                                                                                                                                          Usage
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Best Local S
Matches 122
                                                              SEQUENCE FROM N.A. MEDLINE-89392063; Pub Sato S., Fujita N., F Miyatake T.;
"cDNA cloning and glycoprotein."; Biochem. Biophys.
                                                                                                                                                                                                                                                                                                                                                        MAG_HUMAN
P20916;
                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last seq
15-SEP-2033 (Rel. 42, Last ann
Myelin-associated glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VREPFVRYSYKKSQLSLHVTSLSRTPDIIIPGTLEAGYPSNLTCSVPWACEQGTPPTFSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRKGVSLHEDSPVATSDPRQLVQKATQGRFQLLGDPQKHDCSLFIRDAQKNDTGMYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLWPLPLFLLCAGSLAQDLEFQLVAPESVTVEEGLCVHVPCSVFYPSIKLT-LGPVTGSW
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                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
    Res.
                                            amino
                                                                                                      PubMed=2476987;
                                                                                                                                                                                                                                                                   glycoprotein
                                                                                                                                                                                      Chordata;
Primates;
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Last annotation updat
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  Commun.
                                          acid
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CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE.

IG-LIKE C2-TYPE.

BY SIMILARITY.

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N-LINKED (GLCNAC...) (PC
                                        sequence
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Pred. No. 5.7e-30;
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/FTId=VSP_002534.
; F1FE6D5C393F0FF1 CRC64;
                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQEAITSYNHCLSPTASDAVTPGCSIHRLISRTPRCTAILR

IQDPYRTHLKNRAVSTLREPMISWEGSLRSTGORSKCTKLC

SPYKNLCPLMLPVDNSCIPLITEWYNLLCVSLTLS -> A

QQDSKVHSNPENPRPLQKDSPQEQSSVHTKISLDEMGGKPQ
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163:1473-1480(1989)
                                                                                                                                                                                                                                                                   precursor (Siglec-4a).
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                                                                               Kuwano
                                                                                                                                                                                                                                                                                                                                                                            626
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                                                                                                                                                                                                                                                                                          update)
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                                        human myelin-associated
                                                                               Sakimura
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) (POTENTIAL).
) (POTENTIAL).
                                                                             ...
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                                                                             Takahashi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; 19; 2.

SMART; SM00408; IGC2; 2.

PROSITE; PS50835; IG_LIKE; 3.

Cell adhesion; Lectin; Transm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mediates stalle-acid dependent cell-cell interactions between mediates stalle-acid dependent cell-cell interactions between neuronal and myelinating cells. Preferentially binds to alpha? Ilinked stalle acid (By similarity).

11 SUBUNIT: Binds to RTN4R (By similarity).

12 SUBCELLULAR LOCATION: Type I membrane protein.

13 SUBCELLULAR LOCATION: Type I membrane protein.

14 SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC (STALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.

15 SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.

16 SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
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SEQUENCE FROM N.A.
LAMBERTIN J.E., McCready P.M., Adamson A.W.,
Kyle A., Ramirez M., Stilwagen S.A., Garnes
Bruce R., Quan G., Montgomery M., Ow D., Kob
Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; ipR007110; ig-1ike
InterPro; ipR003598; ig_c2.
InterPro; ipR003006; ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 159460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A61084; A61084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M29273; AAA59545.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases -!- FUNCTION: Adhesion molecule in postnatal neural deve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lmmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; Q62230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AC002132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC: 6783; MAG.
                                Similarity
                                                                                              450
454
531
626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Signal; Glycoprotein;
                                                                                                  MW;
Score 303.5; DB 1;
Pred. No. 5.7e-14;
Prematches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG-LIKE V-TYPE 1.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
                                                                                                                                                                                                        IG-LIKE C2-TYPE 2
IG-LIKE C2-TYPE 3
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Kobayashi A., Ol
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J., Danganan L.,
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15-UUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                           Dulac C.
Roder J.
                                                                                                                                                                                                                                                                                                                                                                                                                       Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMP.
                                                                                            structural similarities within the immunoglobulin superfamily Neuron 8:323-334(1992).
-I- SUBCELULIAR LOCATION: Type I membrane protein.
-I- TISSUB SPECIFICITY: Exclusively expressed by myelinating
                                                                                                                                                                          "Molecular characterization of the structural similarities within the
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
563-571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schwann cell myelin protein precursor
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                                                nonmyelinating schwann cells and oligodendrocytes. DEVELOPMENTAL STAGE: First synthesized at embryonic
  remains expressed SIMILARITY: BELONG
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., le Douarin N.M.;
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-!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
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European Bioinformatics Institute. There are no restrictions on it
by non-profit institutions as long as its content is in no wa
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  PENLRVMVSQAN-----
                                                                                                                         GVSAQRTVRLRVAYAPR--
                                                                                                                                                                                                                      CPP--PSFSWTGA--ALSSQGTK-----PTTSHFSVLSFTPRPQDHDTDLTCHVDFSRK
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                                                                                                                                                                                                                                                                                                        -SQYFFRVERGSYVRYNEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEE
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                                                                          SLSFQADVGLDVQYEPQVVGLWGPTEVVEGSDVELGCEAEGRPAPLISWFRGSEVLREEP
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IPR003598;
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n domain;
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Ig_MHC.
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
BY SIMILARITY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 302.5;
Pred. No. 6.6e
39; Mismatches
                              RTVLEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHWANN CELL MYELIN PROTEIN EXTRACELLULAR (POTENTIAL).
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5.6e-14;
hes 224;
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Gaps

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Db	284	284 GRNLRLLLSNYGPDDGGSFSCVAENRHGRHNRSLQLRVAYAPRAPVING-SLWVYSGDPV 342	342
Qy	287	287 CLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHV 346	346
DЪ	343	343 SVTCRAESEPAAILTVLRGGKVMAAAIYEDHVTMEMRPARPEDGGTYSCVAENQHGASST 4	402
Qy	347	SLSLSVHYKKGLISTAFSTAF	363
Db	403	403 SFNISVEYPPLVLPASRCTAGGDGVRCVCMVNSIPDSSLVFELPTRNQTVSDGHRDFTAA 462	62
Qy	364	SNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRH 406	06
Db	463	463 PPGSDGSITGI-LTLRGPLEPRLLVLCAARNRHGTTARQLREHHPGGLVWAK 513	13
Qу	407	407STILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQ 452	52
Db	514	514 VGPVGAVVAFAIVIAVVCYLSQSRRKKGAGSPEVTPVQPMAGPGGDPDLDLRPQQVRWLR 573.	73.
Оy	453	453 KKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 5	510
В	574	574 GAMERWALGVKEGSGAPQEVTPTSHPPMKPTRGPLEDPPEYAEIR 618	18
Search c	omplet	Search completed: October 8, 2003, 20:03:37	

Search completed: October 8, 2003, 20:03:37 Job time: 22 secs

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Result
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Perfect score:
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2706
1 MLLPLLLSSLLGGS
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Query
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1: sp_archea:
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Listing first 45 summaries
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sp_bacteria:*
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Q8BU57
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Q95JN1
Q15600
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Q95jn1 macaca
Q15600 homo
Q9d4m0 mus
Q9d4m0 homo
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Q8iw38 homo 1
Q8bu57 mus 1
Q9p0f8 homo
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151.5	151.5	152	152.5	153	153.5	155	155	155	155	159	159	159	161	161.5	161.5	161.5	166.5	166.5	166.5	167	167	175	175	175.5	177	182.5	183	184
5.6	5.6	5.6	5.6	5.7	5.7	5.7	5.7	5.7	5.7	5.9	5.9	5.9	5.9	6.0	6.0	6.0	6.2	6.2	6.2	6.2	6.2	6.5	6.5	6.5	6.5	6.7	6.8	6.8
1174	1151	467	373	5636	494	1217	1041	335	213	739	739	650	412	1256	1256	1256	1332	1332	718	468	464	662	510	1252	510	577	483	402
11	11	4	4	4	11	11	4	4	4	δ	σ	σ	6	11	H	1	ۍ	u	υ	4	4	4	4	11	4	1	11	11
Q91Z60	Q9QVN5	Q8NBR8	Q9H6B4	Q96RW7	Q9ESC6	P97685	094856	Q8TCD9	Q8WW91	Q9GKR3	Q28260	Q9GKR2	Q8HY14	Q9ET59	Q9JIX1	Q925S5	Q9VQW7	Q9BN17	Q21139	Q96CA7	Q16170	060926	Q96K15	09ЛІХ2	Q96NY8	Q9D2Z1	09DBP8	035444
Q91z60 rattus norv	5 ratt	Q8nbr8 homo sapien	Q9h6b4 homo sapien	Q96rw7 homo sapien	Q9esc6 mus musculu	5 ratt	094856 homo sapien			Q9gkr3 bos taurus	Q28260 canis famil		. Q8hyl4 oryctolagus			S	Q9vqw7 drosophila	Q9bn17 drosophila	caeno	homo		O60926 homo sapien	Q96k15 homo sapien	ratt	OMO	mus	Q9dbp8 mus musculu	O35444 mus musculu

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8BY18 PRELIMINARY; PRT; 623 AA.
Q8BY18;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Meakly similar to sialic acid-binding lectin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK042488; BAC31272.1; -.
SEQUENCE 623 AA; 69384 MW; 5827C09D52C3AC7F CRC64;
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
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122 RGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSWT
                                                                                                                                                                                       62 KAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 Similarity 43.1 267; Conservative
                                                                                                                                          63 KGIRKPSLSFPVATNNKDKVLEWEARGRFQLLGDISKKNCSLLIKDVQWGDSTNYFFRME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.8%; Score 1211.5; DB
43.1%; Pred. No. 1.3e-96;
tive 55; Mismatches 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111; Indels
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Q8IYH7;
Q1-MAR-2003 (TrEMBLrel. 2:
01-MAR-2003 (TrEMBLrel. 2:
01-MAR-2003 (TrEMBLrel. 2:
SIGLEC-like 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC035809; AAH35809.1; -
SEQUENCE 568 AA; 61977 MW; C955F4D62162B860 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                        IPWDIPVATNTPSGKVQEDTHGRFLLLGDPQTNNCSLSIRDARKGDSGKYYFQVERGSR-
                                                                                                                                                                                                                                                                      LSVNVTASQDLLSRYRLEVPESVTVQEGLCVSVPCSVLYPHYNWTASSPVYGSWFKEGAD
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65; Mismatches 174
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Last annotation update)
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hes 129;
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Q81W38;
Q81W38;
01-MAR-2003
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EMBL; AK036698; BAC29538.1; -
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Weakly similar to sialic acid-binding lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Bone; MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o
                                                                                                                                                                 GAALSSQGTKFTTSHFSYLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVA 235
                                                                                                                                                                                                                                                   RGSYVRYNEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVENWAFEEGPPPSFSWT
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55.1%; Pred. No. 1.7e-49;
56. Mismatches 65;
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Best Local Similarity
                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Oviduct;
MEDLINE-22354683; PubMed-12466851;
The FANTOM Consortium,
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK087658; BAC39955.1; -.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sialic acid-binding lectin SIGLEC-F homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ
EMBL; BC041072; AAH41072.1; -.
NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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                         NCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVTVICVENWAFEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPCSFSYPRQDWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPGAGVTTERTIQLSVSW
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NCSLDIRDAQKIDTGTVFFRLD-GS-VKYSFQKSMLSVLVIALTEVPNIQVTSTLVSGNS
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                                                                                                                                                                                   423 AA;
                                                                                          17.4%;
llarity 29.3%;
Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Chordata; Rodentia;
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                                                                                                                                                                                   45208 MW;
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Pred. No. 8e
                                                                                          Score 471.5; DB 11
Pred. No. 1.7e-32;
9; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                                                                                                                                                7393D0E4BE5BF455 CRC64;
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8e-38;
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                                                                                                                                  DB 11; Length 423;
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; Murinae; Mus
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Query Match
Best Local S
Matches 74
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NON_TER 1 1
SEQUENCE 287 AA.
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InterPro; IPR003006; Ig_MHC.

Pfam; PF00047; ig; 1.
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O9POF8;

01-OCT-2000 (TrEMBLrel. 15,

01-OCT-2000 (TrEMBLrel. 15,

01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Umbilical cord blood;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                                                                                                                                                                    Similarity
                                                                                                                            GAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYN | :|||: :::|: |:||| | | | | | | | :::
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                                                                      FMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSWTGAALSSQG
                                                                                                              GDSMATNNSTQKVQKETQGRFHLLGDPSRNNCSLSIRDARRRDNGSYFFWVAR-RRTKFS
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-- PRTLHSSELTIIPRPQDHGTNLICQVTFPGAGVTTERTIQLSVSW
                       TKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAY 236
                                                     YKYSPLSVYVTALTHRPDILIPEFLKSGHPSNLTCSVPWVCEQGTPPIFSWMSAAPTSLG
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                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GAFLGIGITALLFLCLALII--MKILPKRRTQTETPRPRFSRHSTILDYINVV 416
                                                                                                                                                                     13.7%; Score 371.5; DB 4; 44.3%; Pred. No. 4.9e-24; tive 30; Mismatches 60;
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Last sequence up
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Best Local S
Matches 93
SEQUENCE FROM N.A.
MEDLINE=21523976; PubMed=11546777;
MEDLINE-21523976; PubMed=11546777;
Angata T., Varki N.M., Varki A.;
"A second uniquely human mutation affecting
J. Biol. Chem. 276:40282-40287(2001).
                                                                            Q95KQ0 PRELIMINARY; PRT; 271 AA. Q95KQ0; Q95KQ0; Q1-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) 51alic acid-binding lectin Siglec-L1 (Fragment). Pan paniscus (Pygmy chimpanzee) (Bonobo). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID-9597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Stalic acid-binding lectin Siglec-L1 (Fragment).
Gorilla gorilla).
Gorilla gorilla (gorilla).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
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Angata T., Varki N.M., Varki A.;
Angata T. Varki N.M., Varki A.;
Assecond uniquely human mutation affecting
J. Biol. Chem. 276:40282-40287(2001).
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SMART; SM00409; IG; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                    DESRKGVSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                          LLPPLICGRYGAKEQKD--YLLTMQKSYTYQEGLCVSYLCSFSYPQNGWTDSDPVHGYW
                                                                                                                                                                                                                                                                                                           SS--PVYGSWFKEGADIPWDIPVATNTPGGKVQEDTQGRFLLLG---XPQTNNCSLS--I
                                                                                                                                                                                                                                                                                                                                  EECPPPSFSW--TGA-----ALSSQGTK---PTTSHFSVLSFTPRPQDHDTDLTCHV
                                                                                                                                                                                                                                                                                                                                                          ERGN-MKWNYKYDQLSVNVTASQDLLSRYRLEVPESVTVQEGLCVSVPCSVLYPHYNWTA
                                                                                                                                                                                                                                                                                                                                                                                                             FRAGDHVSRNVPVATNNPARAVQEETRDRFHLLGDPQNKDCTLSIRDTRESDAGTYVFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269
269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                              245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269
30436 MW;
                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 360.5;
Pred. No. 4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96E49E4F779D6E50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     À
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             sialic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sialic acid biology.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
             acid
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                                                                                                    Euteleostomi;
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; Gorilla.
             biology.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                             182
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RESULT 9
Q95KP8
ID Q95K
AC Q95K
AC Q95K
DT 01-1
DT 01-
    QΥ
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Best Local
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                    Angata T., Varki N.M., Varki A.;

A second uniquely human mutation affecting
J. Biol. Chem. 276:40282-40287(2001).

EMBL; AY029757; AAK50564.1; -.

EMBL; AY029756; AAK50564.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pongo pygmaeus (Orangutan),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID-9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC 2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update 01-MAR-2003 (TrEMBLrel. 23, Last annotation update stalic acid-binding lectin Siglec-L1 (Fragment).
                                                                                                                                                                                                                             Pfam; PF00047; 1g; SMART; SM00409; IG;
                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=21523976; PubMed=11546777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q95KP8;
                                                                                                                                                                                   Lectin
                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                               InterPro; IPR003599;
InterPro; IPR007110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q95KP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AY029753; AAK50562.1; -. EMBL; AY029752; AAK50562.1; JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                              90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91;
MLLPLLLSSLLGGSQAMDGREWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                           PS50835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EECPPPSFSW--TGAAL-----SSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                            IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGDHVSRNVPVATNNPARAVQEETRDRFHLLGDPQNKDCTLSIRDTRESDAGTYVFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS--PVYGSWFKEGADIPCDIPVATNTPSGKVQEDTQGRFLLLG---DPQTNNCSLS--I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERGSYVRYNEMNDGFFLKVTA---LTQKPDVYIPE--TLEPGQPVTVICV----FNWAF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLLPPLLCGRVGAKEQKD--YLLTMQKSVTVQEGLCVSVLCSFSYPQNGWTDSDPVHGYW
                                                                                                                                       269
269 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271
271 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                       AΑ;
                                                                                                                                                                                                        IG_LIKE;
                                                                                                                                     269
30649 MW;
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30613 MW;
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                                                                 13.0%;
36.0%;
                                                                                                                                                                                                                                                                     Ig_MHC.
                                                                                                                                                                                                                                                                                             Ig.
Ig-like.
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                                              42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last annotation update)
                                            Score 351.5; DB 6;
Pred. No. 2.5e-22;
2; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 358.
Pred. No.
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                                                                                                                                     D21277346EC3C7CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F63E6018C1C7B934 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358.5; DB 6
No. 6.1e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Pongo.
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                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                        biology.";
                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ω
33;
                                            Gaps
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60
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AB070150; BAB63095.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecinae; Macaca.
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 34.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein SEQUENCE 312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Terao K., Sugano S.;
"Isolation of novel full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Testis;
Hashimoto K., Osada N., Hida M., Kusuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                           250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        HTGNLDEEDCTLLIHDILKGNSATYLFYADLGEQ-KSAFLGENIKLFVSDLTQKPELHIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERGSYVRYNFMNDGFFLKVTA---LTQKPDVYIPE--TLEPGQPVTVICV-----FNWAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGDHVSRNILVATNNPARAVREETRDRFHLLGDPQNKDCTLSIRDTRESDAGTYFFRV
    LAQKRNQKATPNSPRTPLPP 441
                                       GAIAFSLLFFCLVLLLMKMLNWWEEHQSPKTKEGLTLKKPELLEEPEV-------
                                                                            GITA--LLFLCLALIIMKIL------PKRRTQTETPRPRESRHSTILDYINVVPTAGP
                                                                                                                                                                                                                                        LGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLE-LPRV----
                                                                                                                                                                                                                                                                                    TLGCHLNFSLANVTRSSLVKLQVVSPHRLFNSSCS------------
                                                                                                                                                                                                                                                                                                                     DLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPDPPENLRVMVSQANRTVLEN
                                                                                                                                                                                                                                                                                                                                                               EILLAEKPVALNCTLKGTCKEIKALFRSRKNPAVSS-----
                                                                                                                                                                                                                                                                                                                                                                                                    ETLEPGQPVTVICVFNWAFEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DFSRKGVSAQ 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                        VPWANSTINLIGEPEIVMRLRCEGKNQYGI-HTSSFFLIPNKKS-VSSMFVKGLIQGIVY
                                                                                                                                                           -----LEKTVLC-SCSFHGIPTPSVQWWMGG-----VPVDVNSMDNIPRVTSSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDARKGDSGK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS--PVYGSWFKEGADIXWDIPVATNTPSGKVQEDTQGRFLLLG---DPQTNNCSLS--I 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EECPPPSFSW--TGAAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERGN-IKWSYKHDQLSVNVTASQDLLSRYRLEVPESVTVQEGLCXYVPCSVLYPHYNWTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLPPLLCGRVGAKEQKD--YLLTMQKSVTVQEGLCVSVLCSFSYPQDDWTDSDPVHGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34610 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 3.66
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 235.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42CA54C314CC1CF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.6e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.
                                                                                                                                                                                                                                                                                                                                                               -SSSSVPHFILRPEDHGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA
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                                                                               421
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Best Local S
Matches 124
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01-NOV-1996
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q15600;
Q15600;
                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00019; ACTININ_1; 1.

PROSITE; PS50835; IQ_LIKE; 2.

Alternative splicing; Immunoglobulin domain; SIGNAL 1 34 POTENTIAL.

CHAIN 35 430 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan Kobayashi A., Olsen A.S., Carrano A.V.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; X14831; CAA32940.1; -. EMBL; AC004785; AAC18435.1; -. InterPro; IPR007189; Actbind_actnin. InterPro; IPR007110; Ig-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W., Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen Burkhart-Schultz K., Gordon L., Terry A., Garnes J., Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J. Danganan L., Poundstone P., Christensen M., Georgescu A., Avila Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs that code for novel members of the carcinoembryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00213; MYELINPO. SMART; SM00408; IGC2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR000920; Myelin_P0
pfam; PF00047; ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barnett T.R., Kretschmer A Elting J.J., Kamarck M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TM2-CEA
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Colon adenocarcinoma;
MEDLINE-89139550; PubMed-2537311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell Biol.
                      170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298
                                                                                                                                                                                                                      19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor
                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J.E., MCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family.
FEECPPPSFSWTGAALSSOGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT
                                                            QNDTGFYTLQV----IKSDLVNE-----EATGQFHVY----
                                                                                   MQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWA
                                                                                                                                                              GY-WFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKG------NCSLVIRDAQ 109
                                                                                                                                                                                                                      LLTASLL-----TFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQ------LF
                                                                                                                                                                                                                                                             LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVP-----CSFSYPRQDWTGSTPAY
                                                                                                                                           GYSWYKG-
                                                                                                                                                                                                                                                                                                                                                                                  430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108:267-276(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -PSMPEADIPP
                                                                                                                                                                                                                                                                                          7.6%; bu-
22.6%; Pre
73;
                                                                                                                                                                                                                                                                                                                                                                                46910 MW;
                                                                                                                                         -----NRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                 Score 205; DB 4;
Pred. No. 2.5e-09;
3; Mismatches 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307
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                                                                                                                                                                                                                                                                                                                                                                                  195DE9F171D1414F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal;
                                                                                                                                                                                                                                                                                                                                        Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.J.,
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hart J.T.,
                                                                                                                                                                                                                                                                                                     178;
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29;

63

Indels

121;

Gaps

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ACCOMPANDATE ACCOM
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Q9D4M0
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           Query
                                                                                                                                                                                                                                                                                                                                                                                                                                            Arakawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubhi F., Suzuki R., Tomita M., Wagner L., Washio T., Schriml L.M., Staubhi F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Custincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Mordone P. Brog R., Rinnwald M., Rodrinner T., Sakamoro N.
                                                                                                                                                                                                                                                                                                                                      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                         MGD; MGI:1921304; 4931406B18Rik.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                "Functional annotation of a full-length Nature 409:685-690(2001).
EMBL; AK016431; BAB30231.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Testis;
MEDLINE-21085680; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel.
                                                                                                                          Pfam; PF00047;
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              Match
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                                        ; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIYSEVKKQ
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                                                                                                                                              IPR003006; Ig_MHC.
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        Score
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        198.5;
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Matches 102; Conservative
                       SMART; SM00408; IC PROSITE; PS00019;
                                                 InterPro; IPR003006; IPfam; PF00047; ig; 3. SMART; SM00408; IGc2;
                                                                                                                                                                                                                                                                               Kuroki M., Matsuo Y., Misumi Y., Oikawa S., M
"A new isoform of human biliary glycoprotein
encoded by an Alu-like sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barnett 1.A., Kamarck M.E.;
Elting J.J., Kamarck M.E.;
"Carcinoembryonic antigens: Alternative splicing a
"Carcinoembryonic antigens: Alternative splicing a
                                                                                                                                   InterPro; IPR001589;
InterPro; IPR007110;
InterPro; IPR003598;
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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01-MAR-2003
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                                                                                                                                                                                                                                                          Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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                                                                                                                                                                                                                                                     (JUN-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRVAYAPROLVISISRONTPOPPENLRYMVSQANRTYLENLGNGTSLPVLEGQSLCLVCV
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IG_LIKE;
                       ACTININ_1; 1.
                                                                                                                                   Ig-like.
                                                                                                           Ig_MHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 7.5

in Mismatches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1998
01-AUG-1998
01-MAR-2003
SEQUENCE FROM N.A.

Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,

Lamerdin J.E., McCready P.M., Kyle A., Ramirez M., Stilwagen S.,

Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,

Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,

Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,

Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,

Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.

Kobayashi A., Olsen A.S., Carrano A.V.,

"Sequence analysis of a 2.5 Mb region in 19q13.2 containing a

clustered CEA/PSG gene family.";
                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
EuKaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BGP_HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               060430;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                            O8R007 PRELIMINARY; PRT;
O8R007;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last seq
O1-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                        Similar to poliovirus receptor-related Mus musculus (Mouse).
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                           SEQUENCE FROM N.A
                                                                               NCBI_TaxID=10090;
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Similarity 21.2%;
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IPR003006; Ig_MHC
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Sciurognathi; Muridae;
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; ACC04785; AAC18433.1; -. InterPro; IPR001589; Actbind_actnin. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QNDTGFYTLQV-----IKSDLVNE-----EATGQFHVY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYSWYKG--ERVDG-----NRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GY-WFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKG-----NCSLVIRDAQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVP-----CSFSYPRQDWTGSTPAY
KMNEVTYSTLNFEAQQPTQPTSASPSLTATEIIYSEVKKQ
                                                                                                                                                                                                                                                          PRIDSNSWAQAILPSVSQSAEITD--NALPQENGLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEECPPPSFSWTGAALSSOGTKPTTSHFSVLSFTPRPODHDTDLTCHVDFSRKGVSAQRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLTASLL-----TFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQ------LF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRLRVAYAPRDL-VISISRDNTPDPPENLRVMVSQANRT--VLENLGNGTSLPVLE----
                                                         SQEELHYATLNFPGVRP-RPEARMPK--GTQADYAEVKFQ
                                                                                                                             VIGVVALVALIAVALACFLHFGKTGRASDQRDLTEHK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQE----LFIPNITVNNSGSYTCHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -RLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVS-ANRSDPVTLNVTYGPDTPTISPSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -PELPKPS----ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWWINNQSLPVSP---
                                                                                                                                                                                                                                                                                                                       -PRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 194.5;
Pred. No. 2.3
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                                                                                                                                                                                          -PSPESKKNQKKQYQLPSFPEPKSSTQ--APESQE
                                                                                                                                                                                                                                                                                                                                                                                       -NNSVTGCNRTTVKTI-----IVTERQNLTML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-1ike.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; '1g; 2.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC024948; AAH24948.1; -. EMBL; AF472510; AAL79833.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.; "Nectin4/PRR4, a new afadin-associated member of the nectin family that trans-interacts with nectin1/PRR1 through V domain interaction."; J. Biol. Chem. 276:43205-43215(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=21560925; PubMed=11544254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases [2]
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SEQUENCE 508 AA; 55657 MW; 2
                                      434
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                                                                                                                                                            323 PRVQVEHEGEFTCHARHPLGSQHVSLSLSV-----HYKKGLISTAFSNGAFLGIGITAL 376
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395 SIRR-LHSHHSDPRSQPEESVGLRAEGHPDSLKDNSSCSVMSEEPEGRSYSTL 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 AKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 -RGDPDEQVGQVAWARVDPNEGIRELALLHSKYGLHVNPAYEDR-VEQPPPPR-----DP
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                                  SPRTPLPPGAPSPESKKNOKKQYQLPSFPEP-KSSTQAPESQESQEELHYATL 485
                                                                  LLFCLLVVVVVLM------SRYHRRK------AQQMTQKYEEELTLTREN
                                                                                                                                                                                                                                                                                                                                                                                          GQPVT----VICVFNWAFEECPPPSFSW-----TGAALSSQGTKP----TTSHFSVLSFTP 204
                                                                                                         LFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKAT---PN 433
                                                                                                                                                                                                                                                      QANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLEL 322
                                                                                                                                                                                                                                                                                          SRSMNGQPLTCVV--SHPGLLQDRRITHTLQVAFLAEASVRGLEDQN-----
                                                                                                                                                                                                                                                                                                                           RPQDHDTDLTCHVDFSRKGVSAQR--TVRLRVAYAPRDLVISISRDNTPDPPENLRVMVS
                                                                                                                                                                                                                                                                                                                                                               GPPLEEGQGLTLAASCTAEGSPAPSVTWDTEVKGTQSSRSFTHPRSAAVTSEFHLV---P 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRQD------WTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDP 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MPLSLGAEMWGPEA----WLRLLFLASFTGQYSAGELETSDVVTVVLGQDAKLPCFY--
                                                                                                                                             PPLTTEHSGVYVCHVSNELSSRDSQVTVEVLDPEDPGKQVDLVS----ASVIIVGVIAA
                                                                                                                                                                                                                   -----LWQVGR-----EGAT--LKCLSEGQPPPKYNWTRLDGPLPSGVRVKGDTLGF 301
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Search completed: October Job time: 68 secs

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2003, 20:03:11

Title:

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Post-processing: Minimum Match 0%
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seq length: 2000000000
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1 MLLPLLLSSLLGGSQAMDGR.....RPEARMPKGTQADYAEVKFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
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   US-09-038-832-2
US-09-046-736-2
US-08-759-628-4
US-08-759-628-5
US-08-759-628-5
US-08-602-725-32
US-08-602-725-32
US-08-602-725-32
US-08-602-725-32
US-09-638-649-1
US-09-638-649-1
US-09-602-725-36
US-08-08-217-299-1
US-08-389-459A-17
US-08-987-867A-17
US-09-798-326-10
US-09-798-326-10
US-09-778-02-10
US-09-778-510-2
US-08-752-307B-14
US-09-791-326-14
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Sequence 2, Appli
Sequence 4, Appli
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Sequence 31, Appli
Sequence 32, Appli
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Sequence 11, Appli
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Sequence 10, Appli
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Sequence 14, Appli
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US-09-038-832-2
                                                                               ; MOLECULE TYPE: US-09-038-832-2
                                                                                                       TELEFAX: 610-407-0701
TELEX: 846169
INPORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENCTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Applic
; Patent No. 6146845
                    Matches 195;
                                    Best Local Similarity
                                                                                                                                                                                                                 APPLICATION UNMBER: US/09/038,832
FILING DATE: 11-MAR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/041,886
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50018
TELEPHONE: 610-407-0700
TELEPHONE: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ERICKSON-MILLER, CONNIE TITLE OF INVENTION: Sialoadhesin FaTITLE OF INVENTION: (SAF-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. BOX 9
CITY: VALLEY FORGE
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09038832
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P.O. BOX 980
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                    Conservative
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                                 32.8%;
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US-750-141A-2
PCT-US93-00031-23
US-08-261-304-2
US-08-506-296B-21
PCT-US95-08493-13
US-09-724-864-6
US-08-359-705B-8
US-08-457-880A-8
US-08-444-622A-8
US-08-4457-880A-8
US-08-457-880A-8
US-08-457-880A-8
US-08-457-880A-6
US-08-458-646A-8
US-08-458-646A-8
US-08-458-705B-6
US-08-359-705B-6
US-08-359-705B-6
US-08-359-705B-6
US-08-359-705B-6
                    52;
                   Score 888; DB 3;
Pred. No. 9.8e-70;
2; Mismatches 127
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Length 431; Indels

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US-09-038-832-4
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Patent No. 6146845
GENERAL INFORMATION:
                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
            MOLECULE TYPE:
                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0.
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,832
FILING DATE: 11-MAR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-2
TITLE OF INVENTION: (SAF-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                            TYPE: amino a STRANDEDNESS: TOPOLOGY: lir
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                                                                                                                                                   TELEPHONE: 610-407-0701
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CITY: V
                                                                                   LENGTH:
                                                                                                                                                                                                                          NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CONTROL OPERATING SYSTEM: SOFTWARE: FastSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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STREET: P.O. BOX 980
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                                                                                 431 amino acids
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US-09-046-736-2
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                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: KIKLY,
APPLICANT: ERICKSC
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                                                                       REFERENCE/DOCKET NUMBER: GH-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version
CURRENT APPLICATION DATA,
APPLICATION NUMBER: US/09/046,736
FILING DATE: 24-MAR-1998
                                                                                                                                  FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,0
                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
60/041,885
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Sialoadhesin Family Member-3 NUMBER OF SEQUENCES: 4
                                                         TELEFAX:
                                                                                                                                                                                              APPLICATION NUMBER: 60/0 FILING DATE: 02-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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Similarity 47.8%;
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                                                     610-407-0701
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O. Box 980
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Pred. No. 9.8e-70;
2; Mismatches 127;
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                COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VC
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 198;
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                 APPLICANT: Altmann, Scott W.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: MUTATIONAL VARIANTS OF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
ADDRESSEE: DNAX Research Institute
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                                                                                                                                                   STREET: 901 Califo
CITY: Palo Alto
STATE: California
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   APPLICATION NUMBER:
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; Pred. No. 1e-64;
78; Mismatches 174;
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                                  Version
                                       #1.30
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US-08-759-628-5
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Best Local Similarity
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                                                                                    GENERAL INFORMATION:
APPLICANT: Altman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX05520
                 APPLICANT: ROCK, Fernando L. APPLICANT: Bazan, J. Fernando A. APPLICANT: Kastelein, Robert A. TITLE OF INVENTION: MUTATIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 415-852-9196
NUMBER OF SEQUENCES:
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TELEPHONE: 415-496-1200
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TOPOLOGY: 111
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                 MUTATIONAL VARIANTS OF MAMMLIAN PROTEINS
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              Sequence 4, Application US/09046736 Patent No. 6090582
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
FENGTH: 421 amino acids
GENERAL INFORMATION:
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FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,09
REFERENCE/DOCKET NUMBER: [1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COETHADER: PC-TAIL PC-DOS/MS-DOS
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ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
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TOPOLOGY: lir
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STATE: Californ
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                                                                                                                                                           LSWFQGSPALNATPISNTGILELRRVRSAEEGGFTCRAQHPLGFLQIFLNLSVYSLPQLL
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Pred. No. 1.1e-52;
3; Mismatches 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
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APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-3
NUMBER OF SEQUENCES: 4
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REGISTRATION NUMBER: 23
REFERENCE/DOCKET NUMBER:
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TOPOLOGY: lir
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                              YTGKMRPVSGVLL-----GAVGGAGATALVFLSFCVIFIVV---RSCRKKSARP-----
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TILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSS
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                                                                                                                                                                                                                                                                                                                              YFFRVERGSYVRYNEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPP 175
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                                                   ------KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHS
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O. Box 980
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24-MAR-1998
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Pred. No. 3.6e-42;
3; Mismatches 138;
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US-08-408-095-31
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Best Local Similarity
Matches 107; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vo
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,095
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acid
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NAME: Mack, Susan J.
REGISTRATION UNMBER: 30,951
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
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TITLE OF INVENTION: APOPTOPSIS-REGULATING PROTEINS
NUMBER OF SEQUENCES: 35
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CITY: Washington
STATE: D.C.
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TOPOLOGY: linear
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                    314 PSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLS-LSVHYKKGLISTAFSNGAFLGIG 372
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                                                                                                                                                                              SVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPDPPENL 257
                                                                                                                                                                                                                               KPLSE-----IHSGNSVSLQCDFSSSHPK--EVQFFWEKNGRLLG----KESQLNF 212
                                                                                                                                                                                                                                                                     TALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW--TGAALSSQGTKPTTSHF 197
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                                                                                                                RVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPAR----LSWTQRGQVLSPSQ 313
                                                                                                                                                      DSIS----PEDAGS-YSCWVNNS-IGQTASKAWTLEVLYAPRRLRVSMSPGD----- 258
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PHHSQKLRLEPVKVQHSGAYWCQGTNSVGKGRSPLSTLTVYYSPETI-----GRRVAVG
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(202)293-7860
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Pred. No. 2.8e-07;
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; TYPE: PRT
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US-09-638-649-5
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US-09-638-649-5
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SOFTWARE: PatentIn Ve
SEQ ID NO 5
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GENERAL INFORMATION:
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Best Local Similarity 23.3
Matches 101; Conservative
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APPLICANT: Yan, Shi Du
TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 0575/62175
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CURRENT FILING DATE: 2000-08-14
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                                    ----QSEEAEMPE
                                                                            PGVRPRPEARMPK
                                                                                                                                                    QKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNF 487
                                                                                                                                                                                          LGGLGVVALL----
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                                                                                                                                                                                                                                                                                           LPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHY------KKGLISTAFSNGA 367
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                                                                                                                -APESQEDEEE--RAELN- 388
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US-08-602-725-32
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION UMBER: US/08/602,725
FILING DATE: 02-FEB-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/GB94/01816
FILING DATE: 19-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
GB 9317423
FILING DATE: 21-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANCER B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 703-816-4100 INFORMATION FOR SEQ ID NO: 32:
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APPLICANT: BODMER,
APPLICANT: DURBIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REALABLE COMPUTER REALABLE COMPUTER: FILOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
**ADDITICATION NUMBER: US/08/602,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36663 REFERENCE/DOCKET NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: ARLINGTON
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                                                      142 -PELPKPS-----ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWWINNQSLPVSP---
                                                                                                                                                                     110 MQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWA 169
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VRLRVAYAPRDL-VISISRDNTPDDPPENLRVMVSQANRT--VLENIGNGTSLPVLE----
                                                                                                                                     QNDTGFYTLQV-----IKSDLVNE-----EATGQFHVY---
                                                                                            FEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT
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                                                                                                                                                                                                                                                GY-WFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKG-----NCSLVIRDAQ 109
                                                                                                                                                                                                                                                                                      LLTASLL-----TFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQ------LF 63
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1100 NORTH GLEBE ROAD, 8TH FLOOR
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DURBIN, HELGA
SNARY, DAVID
                                                                                                                                                                                                                                                                                                                                                                           Conservative
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BATES, PAUL A
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                                                                                                                                                                                                                                                                                                                                                                   6.2%; Score 167; DB 2; I
23.5%; Pred. No. 2.1e-06;
ative 52; Mismatches 122;
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RESULT 11
US-09-638-649-1
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                                SOFTWARE: Pa
SEQ ID NO 1
LENGTH: 416
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5169835-17
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;SEQ ID_NO:17:
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; APPLICANT: WAI-YEE, CHAN
TITLE OF INVENTION: PREGNANCY SPECIFIC
NUMBER OF SEQUENCES: 48
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/390,409
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                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09638649 Patent No. 6563015
                                                                                                                               APPLICANT: Stern, David M.
APPLICANT: Schmidt, Ann Marie
APPLICANT: Yan, Shi Du
TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AN
FILE REFERENCE: 0575/62175
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Best Local Similarity
Matches 73; Conserv
                                                                                   CURRENT APPLICATION NUMBER: US/09/638,649
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 10
ORGANISM: Bos Taurus
                 TYPE: PRT
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                                                                  PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHAR 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -PELPKPS-----ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWWINNQSLPVSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GY-WFKAVTETTKGAPVATNHQSREVEMSTRGREQLTGDPAKG-----NCSLVIRDAQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -RIQLSNGNRTLTLLSVTRNDTGPYECEIQNPVS-ANRSDPVTLNVTYGPDTPTISPSDT
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US-09-996-243-503
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                                                                                                                                          APPLICANT:
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730p1C13
CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
                                                                          APPLICANT:
                                                                                                           APPLICANT:
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                                                                                       Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                        Stewart,
                                                                                                                                                                                                                                                   Grimaldi, J. Christopher Gurney, Austin L.
                                                                                                                                                                                                                                                                                               Goddard, Audrey
                                                                                                                                                                                                                                                                                                                               Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                              Ferrara, Napoleone
                                                                                                                                                     Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                    Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                 Fong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                Eaton, Dan L
                                                                                                                                                                                                                                                                                                                                                                                            Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                             Botstein, David
                                                                                                                                                                                     Paoni, Nicholas F.
                                                                                                                                                                                                         Pan, James
                                                                                                                                                                                                                   Napier, Mary A.
                                                                                                                                                                                                                                        Kljavin, Ivar
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APPLICATION NUMBER: 60 FILING DATE: 1998-06-1 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-11 APPLICATION NUMBER: 60, FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 APPLICATION NUMBER: 60/088742 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088029 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-03 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/ FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087609 APPLICATION NUMBER: 60/087607 FILING DATE: 1998-06-02 FILING DATE: 1998-05-28 APPLICATION NUMBER: 60/075945 FILING DATE: 1998-02-25 FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088326 FILING DATE: 1998-06-04 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088028 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088025 FILING DATE: 1998-06-04 FILING DATE: 1998-06-02 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/066770 FILING DATE: 1997-11-13 APPLICATION NUMBER: 60/062250 1998-06-10 1998-06-10 1998-05-07 60/088021 60/087827 60/084600 60/088810 60/088738 60/065311 60/049787 60/088734 60/088033 60/088030 60/088026 60/087759 60/087106 60/083322 60/078910 60/065186

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Matches 98
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OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091519
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091626
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091633
OR APPLICATION NUMBER: 60/091978
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FILING DATE: 1998-07-01
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FILING DATE: 1998-06-26
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                                 QA---
 QAYSLVGPEVRGSEPKKVHHANLTKAETTP---SMIPSQSRA
                                                                                                                RVTVQYVQSIGMVA---GAVTGIVAGALLIFLLVWLLIRRKDKERYE-EEERPNEIREDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                          EAPKARLVKPSSSSSGSRSSRSGSSSTRS-
                                                                                  ILDYINVVPTAGPLAQKRNQKATFNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSST
                                                                                                                                       VCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSL
                                                                                                                                                                                                                                                                   TVRLRVAYAPRDLVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCL
                                                                                                                                                                                                                                                                                                                                                                                       MQDESQYFFRVER-GSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                TPAYGYWFKAVTETTKGAPVATNHQSREV----EMSTRGRFQLTGDPAKGNCSLVIRDAQ 109
                                                                                                                                                                             -----PKSRIDYNHPGRVL------LONLTMSYSGLYQCTAGNEAGKESCVV
                                                                                                                                                                                                                                                                                                                             AFEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQR 228
                                                                                                                                                                                                                                                                                                                                                          PSDEGRYTCKVKNSGRYVWSHVI-----LKVLVRPSKPKCELEGELTEGSDLTLQCE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLLLLVSYYVGTLGTHTEIKRVAEEKV-----TLPCHHQLGLPEKDTLDIEW---
                                                                                                                                                                                                                                                                                                                                                                                                                   ------LLTDNEGNQKVVITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                            --PESQESQ-EELHYATLNFPGVRPRPEARMPKGTQA
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18.8%;
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                                                                                                                                                                                                                                                                                                    -SSSGTEPIVYYWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 152.5;
Pred. No. 2.
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                                                      -TANSASRSQRTLSTDAAPQPGLAT
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369
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OR APPLICATION NUMBER: 60/089952
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/090246
OR FILING DATE: 1998-06-22
OR APPLICATION NUMBER: 60/090252
OR FILING DATE: 1998-06-22
OR FILING DATE: 1998-06-22
OR APPLICATION NUMBER: 60/090254
OR APPLICATION NUMBER: 60/090349
OR APPLICATION NUMBER: 60/090349
OR APPLICATION NUMBER: 60/090349
OR FILING DATE: 1998-06-23

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-19 APPLICATION NUMBER:

60/089948 60/089947 6-19

FILING DATE: 1998-06-APPLICATION NUMBER: 60/ FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-18

APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24

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FILING DATE: 1998-06-18

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PRIOR PRIOR

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-17

60/089600

PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17

APPLICATION NUMBER: FILING DATE: 1998-06-APPLICATION NUMBER: 60/089514

60/089532

APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17

DR FILING DATE: 1998-06-12
DR APPLICATION NUMBER: 60/08
DR FILING DATE: 1998-06-16
DR APPLICATION NUMBER: 60/08
DR FILING DATE: 1998-06-16

60/089512 60/089440

RESULT 13 US-09-040-774-2 Sequence 2, Application US/09040774 Patent No. 6207811 GENERAL INFORMATION:
APPLICANT: Tryggv
APPLICANT: Kestil APPLICANT: Tryggvason, Karl Kestila, Marjo Lenkkeri, Ulla Mannikko, Minna Karl

FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-25

APPLICATION NUMBER:

FILING DATE: APPLICATION |

1998-06-

APPLICATION NUMBER:

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-25 APPLICATION NUMBER: 6 FILING DATE: 1998-06-

60/090694 60/090690 60/090678 60/090676

FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090542
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24

APPLICATION NUMBER:

60/090540

FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
FILING DATE: 1998-06-24

APPLICATION NUMBER:

60/090445

APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-24

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RESULT 14
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               Sequence 1, Application US/08217299
PATENT NO. 5672513
GENERAL INFORMATION:
APPLICANT: Mach, J. P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1241 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 300 S.
CITY: Chicago
STATE: IL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff STREET: 300 S. Wacker Drive, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 89; Conserv
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                                                                                                                                                                                 ELPRVOVEHEGEFTCHARHPL--GSQHVSLSLSVHYKKGLI 359
                                                                                                                                                                                                                                                                                      ATARV-----TPRSSDNRQLLVCEASSPALEAPIKASFTVNVLFPPGP
                                                                                                                                                                                                                                                                                                                                                         -KPAPDITILLSGQTIS---
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                                                                                                                                                                                                                                                                                                                                                                                                                       AEYECQVGR-SEMGPELVSPRVILSILVPPKLLLLTPEAGTMVTWVAGQEYVVNCVSGDA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQYFFRVERGSYVRYNFMNDGFFLKVTA----LTQKPDVYIPETLEPGQPVTVICVFNWA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YWFK-----AVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDE 113
                                                                                                                                                                                                                                                    PVLE-----SQSLCLVCVTH-SSPPARLSWTQRGQVLSP-----SQPSDPGVL 320
                                                                                                                                                                                                                  PVIEWPGLDEGHVRAGQSLELPCVARGGNPLATLQWLKNGQPVSTAWGTEHTQAVARSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.6%;
ilarity 22.2%;
Conservative 5
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Pelegrin, A.
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Pred. No. 0.0002;
5; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                       -----DISANVNEGSQQKLFTVE 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OLECUIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/217,29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-MAR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Terskikh, A.
TITLE OF INVENTION: Carcinoembryonic Antigen Derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 9
FILING DATE: 25-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Nutley
                                                                                                                                                                                   156
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            399 PRPRESRHST--ILDYINVVPTAGPLAQKR-----NQKATPNSPRTPL 439
                                               269
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                                                                                                                                                                                                                                                                                    169 AFEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQR 228
                                                                                                                                                                                                                                                                                                                                                      109 QMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNW 168
                                                                                                                                                                                                                                                                                                                      79
                                                                                                                                                                                                                                                                                                                                                                                                                       57 YGY-WFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKG-----NCSLVIRDA 108
                                                                                                                                                                                                                                                                                                                                                                                       29 FGYSWYKG--ERVDG------NRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                           87;
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                                                                                                               SYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQE----LFIPNITVNNSGSYTCQAH
                                                                                                                                                                                                               TVRLRVAYAPRDLVI-SISRDNTPD-PPENLRVMVSQANRTVLENLGNGTSLPVL----
                                                                                                                                                                                                                                                    VYPELPKPS----ISSNNSKPVEDKDAV-AFTCEPETQDATYLWWVNNQSLPVSP--
                                                                                                                                               ---EGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHAR 338
                                                                             HPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTET 398
                                                                                                                                                                                 -- RLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISPLNT
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SYSTEM: PC-DOS/MS-DOS
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s; Pred. No. 0.00043;
53; Mismatches 143;
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                                               -VTTI--
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289 PKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQSLPVSPRLQL 337

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01816
FILING DATE: 19-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9317423
FILING DATE: 21-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,725
FILING DATE: 02-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: YOUNG, SUSAN
APPLICANT: BATES, PAUL A
TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 2220:
                                                                                                                         169 AFEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQR 228
                                                                                                                                                                  109 IQNDTGFYTLHVIKSDLV--NEEATGQFR----- 135
                                                                                                                                                                                                         109 QMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNW 168
                                                                                                                                                                                                                                                    59 FGYSWYKG--ERVDG-----NRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNI 108
                                                                                                                                                                                                                                                                                            57 YGY-WFKAVTETTKGAPVATNHQSREVEMSTRGREQLTGDPAKG-----NCSLVIRDA 108
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                                       TVRLRVAYAPRDLVI-SISRDNTPD-PPENLRVMVSQANRTVLENLGNGTSLPVL---- 281
                                                                                  VYPELPKPS-----ISSNNSKPVEDKDAV-AFTCEPETQDATYLWWVNNQSLPVSP-- 185
6, Application US/08602725 5965710
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DURBIN, HELGA
SNARY, DAVID
STEWART, LORNA MD
                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                   5.3%; Score 143; DB 2; Length 698;
21.3%; Pred. No. 0.00049;
tive 53; Mismatches 143; Indels 126; Gaps
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Sear	Db	Qy	Db	ΩУ	Дb	Qy
Search completed: October 8, 2003, 20:04:44	319 PKPFITS	399 PRPRFSR	299 NS	339 HPLGSQH	244 SYRSGEN	282EGQS
ober 8, 20	NNSNPVEDEDA	HSTILDYIN	DT	IVSLSLSVHYKK	LNLSCHAASNP	SLCLVCVTHSSP
03, 20:04:44	319 PKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQSLPVSPRLQL 367	399 PRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPL 439	299 NSDTGLNRTTVTTITVYAED 318	339 HPLGSQHVSLSUSYHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTET 398	244 SYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAH 298	282EGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHAR 338
			318	398	298	338

Search completed: October 8, 2003, 20:04:44
Job time: 26 secs

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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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     2580.5
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2706
1 MLLPLLSSLLGGSQAMDGR.....RPEARMPKGTQADYAEVKFQ
                                                                                                                                                                                                                                                                                         Match
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       Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compus
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. /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
. /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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. /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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   US-09-910-600-28
US-09-910-600-8
US-09-910-600-8
US-09-978-295A-259
US-09-978-192A-259
US-09-978-189-259
US-09-978-189-259
US-09-978-189-259
US-09-978-189-259
US-09-978-191A-259
US-09-978-585A-259
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Sequence 28, Appl
Sequence 149, App
Sequence 8, Appli
Sequence 259, App
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                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 28
LENGTH: 697
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	ALIGNMENTS				
Sequenc	-10-174-569-	544	83.7	2265	45
Sequen	US-10-173-707-		83.7	26	44
· Sequen	us-10-173-699-		83.7	26	43
Sequen	us-10-173-698-		ω.	26	42
Sequenc	US-10-173		w	26	41
Sequenc	US-10-173-692-		ω.	26	40
Sequenc	US-10-173-691-		ω.	26	39
Sequenc	US-10-173-690-		ω	26	38
Sequenc	us-10-173-689-		ω.	26	37
Sequenc	US-10-196-747-		ω.	26	36
Sequenc	US-10-184-642		ω	26	35
Sequence	US-10-145-128			26	34
Sequence	US-10-194-457		ω	26	33
Sequence	US-10-187-749		ω.	26	32
Sequence	US-10-199-672-118		ω	26	31
Sequence	US-10-143-030A-25		ω	26	30
Sequence	US-10-017-083A-25		ω	26	29
Sequence	US-10-002-967A-25		ω	26	28
Sequence	US-10-143-031A-25		ω ·	26	27
Sequence	US-09-978-298A-25		ω ·	26	26
Sequence	US-09-978-188A-25		ω	26	25
Sequence	US-09-978-375A-25		ω	26	24
Sequence	US-09-978-643A-25		ω ·	26	23
Sequence	US-09-978-187B-25		ω	26	22
Sequence	US-09-978-757A-25		ω.	26	21
Sequence	US-09-999-830		·	26	20
Sequence	US-09-978-193A-25		ω.	26	19
Sequence	US-09-978-423A-25		ω.	26	18
Sequence	US-09-918-585A-25		83.7	26	17
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Sequence 28, Application US/09910600

Publication No. US20030036631A1

GENERAL INFORMATION:
APPLICANT: Longphre, Malinda
APPLICANT: Chang, Han
APPLICANT: Whitney, Gena
TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
FILE REFERENCE: D0003NP CURRENT APPLICATION NUMBER: US/09/910,600 CURRENT FILING DATE: 2001-07-20 PRIOR APPLICATION NUMBER: 60/220,139 PRIOR FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 32 SOFTWARE: Patentin Ver. 2.0 TYPE: PRT ORGANISM: Artificial Sequence FEATURE:

Query Match Best Local Sim Matches 510; 121 ERGSYVRYNEMNDGFELKVTALTQKPDVYIPETLEPGQPVTVICVENWAFEECPPPSFSW 180 61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120 61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120 Similarity 73.2 10; Conservative 95.4%; Score 2580.5; DB 1 73.2%; Pred. No. 3.9e-195; tive 1; Mismatches 1; 1; Indels 185; 11; Length 697, Gaps

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121 181 181

240 240 ERGSYVRYNEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180

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                                           Query Match
Best Local
                                    Matches
                                                                                                              SEQ ID NO 149
                                                                                                                       NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn Ver. 2
                                                                                                                                                                                                                                                                TITLE OF INVENTION: 12 Human Secreted Proteins
                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                   LENGTH: 697
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                                          Similarity
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                                        95.2%;
73.0%;
                             Score 2576.5; DB 11; Length Pred. No. 8.2e-195; 1; Mismatches 2; Indels 1
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RESULT 3 ,
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                                                                                                           CURRENT APPLICATION NUMBER: US/09/910,600 CURRENT FILING DATE: 2001-07-20 PRIOR APPLICATION NUMBER: 60/220,139 PRIOR FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 32 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 8.
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       Query Match
Best Local Similarity
Matches 452; Conserv
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APPLICANT: Chang, Han
APPLICANT: Whitney, Gena
APPLICANT: Whitney, Gena
ITTLE OF INVENTION: NOVEL SIGLECS AND USES
                                                                                                                                                                                                          FILE REFERENCE: D0003NP
                                                                    LENGTH: 544
TYPE: PRT
ORGANISM: Homo sapiens
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     Conservative
                  84.2%;
75.1%;
     1;
                 Score 2278;
Pred. No. 2.
 Mismatches
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.1e-171;
                            Length
                            544;
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RESULT 4
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
                                                                                                                                                                                                                                                                                    Patent No. US2002015
GENERAL INFORMATION:
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APPLICANT:
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                                                                             Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Botstein, David
Desnoyers, Luc
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                                                                                                                                                                                             Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
                                                              Kljavin, Ivar J.
Kuo, Sophia S.
                                       Napier, Mary A.
Pan, James;
                           Paoni, Nicholas F.
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   Margaret Ann
ton, David L.
                                                                                                                                                                           Wei-Qiang
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NUMBER: 60/083742 1998-04-30

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R FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078086
PRIOR APPLICATION NUMBER: 60/078886
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CURRENT APPLICATION NUMBER: US/09/978,697

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

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PRIOR FILING DATE: 1997-10-13

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Baker Kevin P.
Botstein, David
Desnoyers, Luc
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Shelton; David L.
Stewart, Timothy A.
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Gurney, Austin L.
Hillan, Kenneth J
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Wood, William I.
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APPLICATION NUMBER: 60/081955
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APPLICANT: Williams, r. micholand Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630p1C9
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Stewart, Timothy A.
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Botstein, David
Desnoyers, Luc
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                                                                                                       Tumas,
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                                                                                                                                                                                                            vin, Ivar J.
Sophia S.
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Matches 450;
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FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085338
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085323
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APPLICATION NUMBER: 60/085704
FILING DATE: 1998-05-15
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FILING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085582
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                                                                                                                                                          GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP
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                          FQ 512
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2.3e-170;
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RESULT 7 US-09-999-832A-259

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PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/07791
PRIOR FILING DATE: 1998-03-12
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PRIOR APPLICATION NUMBER: 60/078004
PRIOR APPLICATION NUMBER: 60/078806
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PRIOR FILING DATE: 2001-07-30
PRIOR PELICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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Goddard, Audrey
Goddard, Audrey
Godowski, Paul J.
Christopher
Gurney, Austin L.
Gurney, Austin J.
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Williams, P. Mic
Wood, William I.
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Shelton, David L.
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Botstein, David
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Sophia S.
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APPLICATION NUMBER: 60/ FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-01

APPLICATION NUMBER: 60/080333

60/080328

60/080327 60/080194

APPLICATION NUMBER: 60 FILING DATE: 1998-03-

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OR APPLICATION NUMBER: 60/081952
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                                                                                                            APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
FILE REFERENCE: P2630P1C7
FILE REFERENCE: P2630P1C7
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APPLICANT: Baker Kevin P
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Shelton, I
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Grimaldi, J. Christopher
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Desnoyers, Luc
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DR FILING DATE: 1998-03-27
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DR FILING DATE: 1997-11-13
DR APPLICATION NUMBER: 60/066364
DR FILING DATE: 1997-11-21
DR APPLICATION NUMBER: 60/077450
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                            FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/079920
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APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/078939
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APPLICATION NUMBER: 60/078936
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Sequence 259, Application US/09978608A
Publication No. US20030045462A1
GEMERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Pred. No. 2.3e-170;
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LENGTH: 544
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391 KRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK
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Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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Pred. No. 2.3e-170;
1; Mismatches 3;
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C15
FILE REFERENCE: P2630P1C15
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/978,585A CURRENT FILING DATE: 2001-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 624
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APPLICANT: Baker Kevin P.
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          121 ERGSYVRYNEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180
                                                          61
                                                             61 FKAVTETTKGAPVATNHOSREVEMSTRGREQLTGDPAKGNCSLVIRDAQMQDESQXFFRV 120
                                                                                                                    1 MLLPLLLSSLLGGSQAMDGREWIRVQESYMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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ERGSYVTYNFMNDGFFLKVT---
                                                 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVTRDAQMQDESQYFFRV
                                                                                                      MLLPLLLSSLLGGSQAMDGREWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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Shelton, David L.
Stewart, Timothy A.
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Kuo, Sophia S.
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Gao, Wei-Qiang
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D. US20030049633A1
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                                                                                                                                                                             83.7%;
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                                                                                                                                                             Score 2265; DB 11;
Pred. No. 2.3e-170;
1; Mismatches 3;
                                                                                                                                                              Indels 148;
                                                                                                                                                                                       Length
                                                                                                                                                            Gaps
                                                 120
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H 7 H H H R 7 7	APPLICANT: Hillan, Kenneth J APPLICANT: Kljavin, Ivar J. APPLICANT: Kuo, Sophia S. APPLICANT: Nuo, Sophia S. APPLICANT: Napier, Mary A. APPLICANT: Pan, James; APPLICANT: Panni, Nicholas F. APPLICANT: Roy, Margaret Ann APPLICANT: Shelton, David L. APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A.	APPLICANT: Baset Neville. APPLICANT: Beststein, David APPLICANT: Desnoyers, Luc APPLICANT: Eaton, Dan APPLICANT: Ferrara, Napoleon APPLICANT: Filvaroff, Ellen APPLICANT: Fong, Sherman APPLICANT: Goo, Wei-Qlang APPLICANT: Gerber, Hanspeter APPLICANT: Gerber, Hanspeter APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANT: Goddard, J. Christopher APPLICANT: Grimaldi, J. Christopher APPLICANT: Grimaldi, J. Christopher	O 0 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	Qy 391 KRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK 450	271 NIGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTORGOVLSPSOPSDPGVLELPRVOVEHE	Qy       181 TGAALSSQGTKPTTSHFSVLSETPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240         Db
PRIOR FILLING DATE: 1998-04-08 PRIOR APPLICATION NUMBER: 60/081071 PRIOR FILING DATE: 1998-04-08 PRIOR PRIOR FILING DATE: 1998-04-08 PRIOR APPLICATION NUMBER: 60/081195 PRIOR FILING DATE: 1998-04-08 PRIOR FILING DATE: 1998-04-08 PRIOR FILING DATE: 1998-04-09 PRIOR FILING DATE: 1998-04-09 PRIOR FILING DATE: 1998-04-09 PRIOR FILING DATE: 1998-04-09	APPLICATION N FILING DATE: APPLICATION N	APPLICATION NUMBER: 6 FILING DATE: 1998-03-	FILING DATE: 1998-0: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-0: APPLICATION NUMBER: FILING DATE: 1998-0: APPLICATION NUMBER:	AFFERE	APPLICATION NUMBER: FILING DATE: 1998-03	PRIOR FILING DATE: 1997-10-17  PRIOR APPLICATION NUMBER: 60/064249  PRIOR FILING DATE: 1997-11-03  PRIOR FILING DATE: 1997-11-13  PRIOR FILING DATE: 1997-11-13  PRIOR FILING DATE: 1997-11-21  PRIOR FILING DATE: 1997-11-21  PRIOR APPLICATION NUMBER: 60/077450  PRIOR FILING DATE: 1998-03-10  PRIOR FILING DATE: 1998-03-11  PRIOR FILING DATE: 1998-03-11

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OR FILING DATE: 1998-04-29

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OR APPLICATION NUMBER: 60/08358

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OR APPLICATION NUMBER: 60/08359

OR FILING DATE: 1998-04-29

OR FILING DATE: 1998-04-29

OR FILING DATE: 1998-04-30

OR APPLICATION NUMBER: 60/083742

OR APPLICATION NUMBER: 60/083742

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OR APPLICATION NUMBER: 60/084366

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OR FILING DATE: 1998-05-05

OR APPLICATION NUMBER: 60/084366

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OR APPLICATION NUMBER: 60/084637
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084639
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OR APPLICATION NUMBER: 60/084640
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084598
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OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082797
OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082796
OR FILING DATE: 1998-04-23
OR APPLICATION NUMBER: 60/083336
OR FILING DATE: 1998-04-27
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083495
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OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/081819
OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/081952
OR FILING DATE: 1998-04-15
OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/081838
OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/082568
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082568
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/
FILING DATE: 1998-05-07
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FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084441
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APPLICATION NUMBER: 60/
FILING DATE: 1998-04-22
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FILING DATE: 1998-04-21
APPLICATION 1000BER: 60/
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                                                 60/085338
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OR APPLICATION NUMBER: 60/085582
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085700
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085689
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085579
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085573
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                                                           511
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FILING DATE: 1998-05-15
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                                                                          GEFTCHARHPLGSOHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP
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                                                                                                                                                                                                                                                                                                                                  TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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Pred. No. 2.3e-170;
1; Mismatches 3;
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Sequence 259, Application US/09978403A Publication No. US20030050240A1 GENERAL INFORMATION:

APPLICANT: Ashkenazi, APPLICANT: Baker Kev

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APPLICANI: TUMBS, Daniel
APPLICANI: Williams, P. Mickey
APPLICANION WINDER: US/09/978.403A
CURRENT PILLING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062361
PRIOR APPLICATION NUMBER: 60/06311
PRIOR APPLICATION NUMBER: 60/06311
PRIOR APPLICATION NUMBER: 60/06364
PRIOR APPLICATION NUMBER: 60/076311
PRIOR APPLICATION NUMBER: 60/076311
PRIOR APPLICATION NUMBER: 60/07631
PRIOR APPLICATION NUMBER: 60/07632
PRIOR APPLICATION NUMBER: 60/077632
PRIOR APPLICATION NUMBER: 60/077632
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077649
PRIOR APPLICATION NUMBER: 60/077896
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079936
PRIOR APPLICATION N
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APPLICANT:
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerritsen,
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Desnoyers, Luc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           James ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mary A.
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f, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mary E.
60/079786
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OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082797
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OR APPLICATION NUMBER: 60/082796
OR FILING DATE: 1998-04-23
OR APPLICATION NUMBER: 60/083336
OR FILING DATE: 1998-04-27
OR APPLICATION NUMBER: 60/083322
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OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/081952
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FILING DATE: 1998-03-31
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FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/085697
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
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FILING DATE: 1998-05-13
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FILING DATE: 1998-05-13
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APPLICATION NUMBER: 60/084639
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                                                                  LVISISRDNTPD----
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                                                                                                                                 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
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Pred. No. 2.3e-170;
1; Mismatches 3;
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CURRENT APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065364
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-13
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C25
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Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Shelton, David L.
Stewart, Timothy A.
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Kuo, Sophia S.
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Desnoyers, Luc
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PRIOR APPLICATION NUMBER: 60/077450
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR PRILING DATE: 1998-03-26
PRIOR PRILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079668
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079668
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PRIOR APPLICATION NUMBER: 60/079768
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PRIOR APPLICATION NUMBER: 60/079728
PRIOR APPLICATION NUMBER: 60/080105
PRIOR APPLICATION NUMBER: 60/080107
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US-09-999-833A-259
Sequence 259, Application US/09999833A; Publication No. US20030054405A1; GENERAL INFORMATION:
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        APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Faton, Dan
APPLICANT: Filvaroff, Elle
APPLICANT: Filvaroff, Elle
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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Matches
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Botstein, David
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                                      Filvaroff, Ellen
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       Wei-Qiang
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Pred. No. 2.3e-170;
1; Mismatches 3;
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CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR PRIOR DATE: 1997-10-17
PRIOR PPLICATION NUMBER: 60/062250
PRIOR PRIOR DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066364
PRIOR APPLICATION NUMBER: 60/0677450
PRIOR FILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-10
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Tra
TITLE OF INVENTION: Acids Encoding
FILE REFERENCE: P2630P1C65
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OR FILING DATE: 1998-03-30
OR APPLICATION NUMBER: 60/080105
OR FILING DATE: 1998-03-31
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
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Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
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Grimaldi, J. Christopher
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Hillan, Kenneth J
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271 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
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                                                                                                                LVISISRDNTPD----
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                                                                                                                                                        TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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                                     WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
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                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/981/915A CURRENT FILING DATE: 2001-10-16 PRIOR APPLICATION NUMBER: 09/918585 PRIOR FILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: 60/062250 PRIOR APPLICATION NUMBER: 60/062250 PRIOR FILING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: 60/064249 PRIOR FILING DATE: 1997-11-03
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Sequence 259, App
Publication No. 1
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FILE REFERENCE: p2630p1C12
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Tumas, Daniel
Tumas, P. Mickey
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Grimaldi, J. Christopher
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Hillan, Kenneth J
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                                     NOKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK
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-Q-/cgn2_1/USPYO_spoo1/US09937636/runat_08102003_083236_29962/app_query.fasta_1.711
-DB-GenEmb1 -OFMT-fastap -SUFFIX-p2n.rge -MINNATCH-0.1 -LOOPCL-0 -LOOPEXY-0
-UNITS-b1ts -START=1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MIX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-2 -MALIEN-2000000000
-USER-US09937636_@CGN_1_1_3635_@runat_08102003_083236_29962 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -MAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEDUT-120 -MARN_TIMEOUY-30 -THREADS-1 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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BLOSUM62
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

Qy ,	Qy :	Qy Db 2:	US-09-937-636-3	Query Match: DB:	Percent Similarity: Best Local Similarity:	Pred. No.:	Alignment s	BASE COUNT									CDS	gene		source	FEATURES	TITLE	REFERENCE	JOURNAL MEDLINE	TITLE	AUTHORS	REFERENCE	SOURCE ORGANISM	VERSION KEYWORDS	ACCESSION	AF311905
41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60 	21 PheTrpIleArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40	1 MetLeuLeuProLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20 	36-3 (1-512) x AF311905 (1-3124)	96.648	84.398 Conservative:	Length:	OOTBG.	769 a 910 c 813 g 632 t	AGPLAQKRNQKATENSPETPLEGGAPKATLEKKNKKQYQLPSFPEPKSSTQAPESQES	TARGORAFICATIVAL TO CLASS THAN TO ACCOMPENDATE OF THE CONTROL OF T	ADDSQPPATESWYLQARVESSHPWGPRPLGEELPGVKAGDSGRYTCRAERREGGRACE ANDSQPPATESWYLQARVESSHPWGPRPLGEELPGVKAGDSGRYTCRAERREGGRASS	TVICVENNAFEECCPPESTSWTGAALSSQGTROFF THE FSVLETPREQDHATDLTCAFF V FSVRGVVVQAPTURE TO THE TOTAL STATE THE SULFT FREQUENT FAVORAGE TO THE TOTAL STATE THE SULFT FREQUENT FAVORAGE TO THE TOTAL STATE THE SULFT FREQUENT FAVORAGE TO THE SULFT FREQUENCY OF THE SULFF FREQUENCY OF THE SULFT FREQUENCY OF THE SULFORM OF THE SULFT FREQUENCY OF THE SULF FREQ	YPRODWIGSTPAYGYWEKAVTETTKGAPVATHQGSREVEMSTRGREDLYV DEGILEDGAKGNCS	/db_xref="GI:15217166" /db_xref="GI:15217166" /trans]afion="MILDVILESTIAGGOAMDGBEWIDDORGVANDEGIOTSVDOGEG	/product="sialic acid-binding Ig-like lectin 10" /protein id="AAK99542 1"	/noter siglec-10; similar to other siglec family members"  /nodon start=1	2332031 2032031	13124 Cannot 1990 13124 (Apple 1991) 1990	406 T		Medical University, 800 Xiangyin Rd., Shanghai 200433, P.R.China Location/Qualifiers	lang, w., wan, T. and Cao, x.  bmission  1/15-ANG-2001) Department of	1 to 3124)		Cady Cloning and characterization of Siglec-10, a novel sialic acid binding member of the Ig superfamily, from human deadrific cells	T., Zhang,J., C	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3124)	ıs (human ıs	AF311905.1 GT:15217165	complete cds.  AF311905	3124 bp mRNA linear PRI 21-AUG
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Alignment Scores: 7.3e-142 Length: 2208 Pred No.: 2580.50 Matches: 510 Score: 2580.50 Matches: 510 Percent Similarity: 73.31% Conservative: 1 Best Local Similarity: 73.17% Mismatches: 1 Query Match: 95.36% Indels: 185 DB: 6 Gaps: 2 US-09-937-636-3 (1-512) x Ax365530 (1-2208)		1783 451 1843 1947 1903 491 1963 511 2023	Oy  331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerglnHisValSerLeuSerLeu 350
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Yan,W.P. and Longphre,M.
A new Siglec family member, SIGLEC10, is expressed
immune system and has signaling properties similar
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Longphre, M., Whitney, G.S.,
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331 GlyCluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350	1318 CCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAGCACGAA 1377	311 ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGluHisGlu	1258 GTCACACACAGCCCCCCCAGCCAGCCTGAGCTGGACCCCAGAGGGGACAGGTTCTGAGC 1317	8 AACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTGGTCTGT	71 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCys	38 CAGTATCCTCCAGAGACCTGAGAGTGATTCCCCAAGCAAACAGGACAGTCCTGGAA	253ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu	1078 TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTG 1137	18 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC 10	252 252	958 CAGCCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCCTCCCATCCC 1017	252 252	898 GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCTGACAGC 957	252 252	232 41 Leuvallieber Leberar gaspashini Froasp 41 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1		221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240	718 AGCTTCACGCCCAGACCCCAGGACCACAACACCGACCTCACCTGCCATGTGGACTTCTCC 777	SerPheThrProArgProGlnAspH1sAspThrAspLeuThrCysH1sValAspPheSer 2		81 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 20	161 ThrVallleCysValPheAsnTrpAlabheGluGluCysProProProSerPheSerTrp	GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACCCCTGGAGCCCGGGCAGCCGGTG 5	141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 160	478 GAGAGAGGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTTTCT	121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140	418 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 477	101 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 120	358 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC 417	81 GluvalGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 100		
/org /mol	FEATURES Location/Qualifiers source 13024	Patent: WO 0208257-A 27 31- BRISTOL-MYERS SQUIBB COMPAN	REFERENCE 1  AUTHORS Longphre,M., Chang,H. and Whitney,G.	SOURCE synthetic construct ORGANISM synthetic construct	AX365542	LOCUS AX365542 3024 bp DNA linear PAT 15-FEB-2002 DEFINITION Sequence 27 from Patent W00208257.		Db 2158 GCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCCAA 2208	496		A76 CardinglinglinianHictoryanicontendendiatoryanatoryanatoryanging	OY	1978 CORRECCCIVITCACCACCACCACCACCACCACCACCACCACCACCACCAC	436 ArgThrProLeuProProGLyAlaProSerProGluserLySLySASnoinLySLySGIn	1918 GTCCCGACGCTGGCCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACACAAACAGTCCT	Qy 416 ValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerPro 435	1858 ACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCACGATCCTGGATTACATCAATGTG	415	_	1738 AAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGGCATCACGGCT	Qy 356 LysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThrAla 375	Db 1678 TGTGAGGCCTGGAACGTCCATGGGGCCCAGAGTGGATCCATCC	355Lys	CCCTGGGCCAACAGCTCCCTGAGCCTCCATGGAGGGCTCAGCTCCGGCCTCAGGCTCCGC	354	Oy 354	1498 CACITGUAGCITGUICCUAGGUUAGGUUGGUUCCUTUTUTGUGGUTTGGUTTGGGAAA 13	354	1438 TCCGTGCACTACTCCCCGAAGCTGCTGGGCCCCTCCTGCTCCTGGAAGGCTGAAGGGTCTG 14	351 SerValH1sTyr	Db 1378 GGAGAGTTCACCTGCCACGCTCGGCACCACTGGGCTCCCCAGCACGTCTCTCAGCCTC	

252 25	Qy 252 252  Db 909 GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCTGACAGC 968	Qy 241 LeuVallleSerIleSerArgAspAsnThrProAsp 252	Qy 221 ArgLysGlyValSerAlaGinArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240	Qy 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220	Qy 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200	Qy 161 ThrVallleCysValPheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp 180	Db 549 GCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACCCTGGAGCCCGGGCAGCCGGTG 608	489 GAGAGAGGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTTTCT	Qy 121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140	429 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 4	10   Casterimina   Learn   John Not C   Discreting and Delantary   1	Qy 81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 100 	Qy 61 PheLysalaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80	Qy 41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60	Qy 21 PheTrpI1eArgYalGlnGluSerValMetValProGluGlyLeuCysI1eSerValPro 40		<pre>1 MetLeuLeuProLeuLeuSerSerLeuLeuGlyGly</pre>	95.36% Indels: 6 Gaps: 6 Gaps: 2) x Ax365542 (1-3024)	nt Similarity: 73.31% Conservative: 1	ed. No.: 1.05e-141 Length: ore: 2580.50 Matches:	Alignment Scores.	ASE COUNT 699 a 933 c 790 g 602 t	/db_xref="taxon:32630"
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Db RESULT AX36551	Qy	Qy	Db S	2 B 5	Q	Db	P 5	מ מ	0 B	Qy Db	VQ	pb Qy	Db	O <sub>V</sub>	рь Оу ,	Db Oy	Db	Qy	Qy dd	Db .5	O D
2078 GCC	496 AlaArgMetDroLysGlyThrGlnAlaAspTyrAlaGluValLysPheGln 512	4/6 SerdingludiuLeuHisTyralaThrLeuAsnPheProGlyValArgProArgProGlu 495	### ATTCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCCCAGGG 2	THE CONTROL OF THE CO	4.16 VALPYOYDEA AGLYYFOLEHAIAG INLYSAGASGINLYSALATINFYDASGASGEFFTO 4.35	THE STUTH FERM SET OF SET AS SET FIRE THE SET OF THE		76 Leulen Dhelen Custen al atout lette wett wette eine grotugargargargard. 3		1538 CCCTGGGCCAACAGCTCCCTGAGCCTCCATGGAGGGCTCAGCCTCTGGCCTCAGGCTCCGC 1597	A	354 354  1478 GAGGTGGTGGAGGGGAACAGCAGGCCAGGACTCCATTCGAGGTCACCCCCAGCTCAGCCGGG 1537	18 CACTGCAGCTGCTCCCCAGGCCAGCCCGGCCCCCTCTCTGCGCTGGTGGCTTGGGGAG 14	54	351 SerValHisTyr	331 G.YGLUPheThrCY9H18ALAArgH.sProLeuGLYSerGINH1SVaLSerLeuSerLeu 350 	38 CCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAGCAGGAA 12	311 ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGluHisGlu 330	291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310	AACCTTGGGAACGCACGTCTCCCAGTACTGGAGGCCAAAGCCTGTGCCTGGTCTGT	
		D Qy	Qy	Qy	Qy	Qy Db	Qy Db	Qy Db	Db :	Qγ Db	US-09-937-0	Mat	: nt S Loca	Alignment : Pred. No.:	BASE COUNT ORIGIN	source	FEATURES	AUTHORS TITLE JOURNAL		KEYWORDS SOURCE ORGANISM	LOCUS DEFINITION ACCESSION VERSION
	181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu	161 ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp	141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal	121 GluargGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 	101 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 	81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn	61 PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg	41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 	21 PheTrpIleArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro	1 MetLeuleuFroLeuLeuleuSerSerLeuleuGlyGlySerGinAlaMetAspGlyArg 		h: 84.18% 6	milarity: 75.25% Conservative: 1 Similarity: 75.08% Mismatches: 1	Length: 25	627 a	Ф	BRISTOL-MYERS SQUIBB COMPANY (US) Location/Qualifiers	Longphre, M., Chang, H. and Whitney, G. Novel siglecs and uses thereof Patent: WO 0208257-A 1 31-JAN-2002;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;	Homo sapiens	AX365516 2565 bp DNA linear Sequence 1 from Patent WOO208257. AX365516 AX365516
  GTGCTC 554   alaspPheSer 220		erPheSerTrp 180	lyGlnProVal 160	euLysValThr 140             TAAAAGTAACA 548	hePheArgVal 120             TCTTTCGGGTG 488	laLysGlyAsn 100               CCAAGGGGAAC 428	isGlnSerArg 80             ACCAGAGTCGA 368	YrGlyTyrTrp 60             ATGGCTACTGG 308	leSerValPro 40              TCTCTGTGCCC 248										<pre>Euteleostomi; ; Homo.</pre>		PAT 15-FEB-2002

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                                                                                             ThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGluSerLysLys
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                                              AsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAla
                                                                                                                             GATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGAAAGCC
                                                                                                                                           AspTyrIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla
                                                                                                                                                                                                                                                                                                                                                            CCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAGCACGAA
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                                  AACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCCAGAACCCAAATCATCCACTCAAGCC
                                                                                 AGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCCTATGCCCCCCAGAGAC
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AX376050
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Gurney,A.L., Pan,J.,
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GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr
                                               CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal
                                                                                            GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLySGlyAsn
                                                                                                                           PheLysalavalThrGluThrThrLysGlyAlaProvalAlaThrAsnH1sGlnSerArg
                                                                                                                                                                          MetLeuLeuProLeuLeuSeuSerSerLeuLeuGlyGlySerGlnalaMetAspGlyArg
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                                                                                 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC
                                   TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG
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/db_xref="taxon:9606"
798 c 717 g
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/mol_type="genomic DNA"
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Primates;
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.eGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuPro 390 	IleG	371 1252
ilsTyrLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370                       ACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGA 1251	SerV	351 1192
heThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350 	GlyG      GGAG	331 1132
InProSerAspProGlyValLeuGluLeuProArgValGlnValGluHisGlu 330 	ProS	311 1072
ilsSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310 	0-4	291 1012
:lyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCys 290 	ASnL      AACC	271 952
YOPYOGIUASNLEUAT GVAlMETVALSETGINĀLAASNAT GTĪTVALLEUGIU 270 	CAGT	253 892
GCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTG 891	TACA	832
252	] ] 4	252
CTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC 831	TGGG	772
252	1	252
CTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCCCATCCC 771	CAGC	712
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252	;	252
leSerIleSerArgAspAsnThrProAsp252 	CTTG	241 592
SLYVALSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240 	ArgL:      AGAA	221 532
hrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220 	SerP	201 472
\laAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200	Thre	181 466
465		465
leCysValPheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp 180	Thrv	161
465	1 1	465
hrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 160	AlaL	141
GAAGCTATGTGACATATAATTTCATGAACGATGGGTTCTTTCT		406
		AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal  AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal  ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProProFroSerPheSerTyp  ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerTyl

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 ${\tt MetLeuLeuProLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg}$ 

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Mammalla; Eutherla; Primates; Catarrhini;
1 (bases 1 to 3099)
1 (bases 1 to 3099)
1 (bases 1 to 3099)
1 (kikly K.K. and Miller.C.L.E.
Sialoadhesin family 4(SAF-4) cDNA
Patent: JP 2001502359-A 1 20-FEB-2001;
PATENTINE BEECHAM CORP
OS HOMO Sapiens (human)
PN JP 2001502359-A/1
PD JP-2001502359-A/1
PD 20-FEB-2001
PF 27-MAY-1998 JP 1999500864
PR 27-MAY-1997 US 60/047572
PI KRISTINE KAY KIKLY.CONNIE LYNN ERICK
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PF 27-MAY-1998 JP 1999500864

PR 27-MAY-1997 US 60/047572

PI KRISTINE KAY KIKLY, COUNIE LYNN ERICKSON MILLER PC

A61K38/00,A61K39/395,A61K48/00,C07H21/04,C07K14/435,C07K14/705, PC

C07K16/00,

PC C07K16/18,C07K16/28 C12N15 / 2 - 7
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Sialoadhesin family 4(SAF-4) cDNA.
BD011516
BD011516.1 GI:18639889
JP 2001502359-A/1.
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                                                                                                                                                                     a
                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
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908 c 813 g 60
                                1.11e-120
2220.50
64.99%
64.85%
82.06%
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VERSION KEYWORDS	DEFINITIO	BD011517 LOCUS	٥	D &						ОУ			₽ &			Ф	Qy	Дb	Qy	рь	Qy	Db	Qy	da	Qy			문 5					Db
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Oy 161 ThrVallleCysValPheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp 180	141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 1	Qy 121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140			61 231	Qy 41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60	21 111	OS-09-93/-636-3 (1-512) x BUTLIST/ (1-5099)  Oy 1 MetLeuLeuProLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20  Oy 1	ary Match:  82.06% Indels:  Gaps:  Co-037.636.2 (1.612) x pholific (1.3000)	Pred. No.: 1.11e-120 Length: 3099 Score: 220.50 Matches: 452 Percent Similarity: 64.99% Conservative: 1 Per Conservative: 1	Scores:	BASE COUNT 769 a 908 c 813 g 607 t 2 others ORIGIN	source	FH Key Location/Qualifiers  FT source 13099  FT /Organism-'Homo sapiens (human)'.  FEATURES Location/Qualifiers	A61K38/00, A61K39/395, A61K48/00, C07H21/04, C07K14/435, C07K14/705, PC C07K16/00, C07K16/00, C07K16/00, C12N15/11, C12N15/12, C12N15/63 CC	PD 20-EBS-2001  PD 20-EBS-2001  PF 27-MAY-1998 JP 1999500864  PF 27-MAY-1997 US 60/047572  PR 27-MAY-1997 US F6/047572  PI KRISTINE KAY KIKLY, CONNIE LYNN ERICKSON MILLER PC	JOURNAL Patent: JP 2001502359-A 2 20-FEB-2001; SMITHKLINE BEECHAM CORP COMMENT OS Homo sapiens (human) DN TD 2001502359-A /2	REFERENCE 1 (bases 1 to 3099)  AUTHORS Kikly,K.K. and Miller,C.L.E.  TITLE Sialoadhesin family 4(SAF-4) CDNA	;hordata; Craniata; Vertebrata; F
Qy 355Lys 355	<sub>L</sub>	Db 1317 GAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCTCAGCCGGG 1376	Db 1257 CACTGCAGCTGCTCCCCAGGCCCAGGCCCCCCTCTCTGCGCTGGTGGCTTGGGGAG 1316  Qy 354 354	ы	TGCCACGCTCGGCACCCACTGGGCTCCCAGCACGTCTCTCAGCCTC	1077 CCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCCAAGTGGAGCACGAA	291 1017	271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCySLeuValCys			777 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTAAGGCTAAGGCTGAAGGCTAAGGCTAAGGCTAAGAAGGCTGAAGGCTAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	252	Db 717 CAGCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCCTCGTCCCATCCC 776	GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCTGACAGC	QY 241 LeuVallleSerIleSerArgAspAsnThrProAsp	5 2			Db 470 470

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Kitzig,Fr., Martinez-Barriocanal,A., Lopez-Botet,M. and Sayos,J.
Cloning of two new splice variants of Siglec-10 and mapping of
interaction between Siglec-10 and SHP-1
Biochem. Biophys. Res. Commun. 296, 355-362 (2002)
                                                                                                                                                                            Direct Submission
Submitted (17-APR-2001) Immunology, Universitat Pompeu Fabra (CEXS), Dr. Aiguader No. 80, Barcelona 08003, Spain
                                                                                                                                                                                                                                                                                                                                                        2126 bp mRNA linea
Homo sapiens sialic acid-binding protein splice
(Siglec-10 Sv3) mRNA, complete cds.
AY032685
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Kitzig, F., Alvarez-Errico, D.,
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                          sapiens (human)
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157. .2076
                                                                                                                    /organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="19"
                                                      /gene="Siglec-10
/codon_start=1
                                                                                                         /map="19q13.3"
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                                            ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp
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                                 AGAAAGGGTGTGAGCGTACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCCAGAGAC
                                                                           AGCTTCACGCCCAGACCCCAGGACCACAACACCGACCTCACCTGCCATGTGGACTTCTCC
                                                                                                                                       ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu
                                                                                                                                                                                  ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp
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IVIRDAQMQDESQYFFRVERGSYVRYNEMNDRFFLKVTVLSFTPRPQDHNTDLTCHVD
FSRKGYSVQRTVRLRVAYAPRDLVISISBDNTPALEPQPQGNUYYLEAQXGQFLRLLC
RADSQPPATLSWYLQNRYLSSSHPMGPRPLELELPGVKAGDSGRYTCRAENRLGSQGF
ALDLSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCIVCVTHSSPPARLSW
TQRGQVLSPSQPSDPGVLELPRVQVEHGGEFTCHAFPUGSGHVSLSBYHYSPKLLG
PSCSWEAEGLHCSCSSQASPAPSLRWMIJGEELLEGNSSQDSFFVTPSSAGPMANSSLS
LHGGLSSGLRLRCEASNAVHGAQSGSILQLPDKKGLISTAFSNGAFLGIGITALLFLCL
ALIIMKILPKRRTQTETPRPRFSRHSTILDYINVPTAGPLAQKRNQKATPNSPRTPL
PPGABSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQLEHYATLNFPGVRPRPEAR
MPKGTQADYAEVKFQ"

593 g (1-2126)Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 2126 448 1 5 243

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1303 TÜCĞİĞCACTACTCCCGGAAGCTGCTGGGCCCCTCTGGGAGGCTGAGGGTCTG 1362 354	CAGTATCCTCCAGAGCACCCCCCGGGGTTCCAGGCTCCAGCCCCCCCC	703 CTTGTTATCAGCATTTCACGTGACAACACGCCAGCCCTGGAGCCCCAGGCCAAT 762 252
Alignment Scores:  Pred. No.:  2142.50  Matches:  243  Score:  2442.50  Matches:  435  Percent Similarity:  63.97%  Mismatches:  1  Best Local Similarity:  63.97%  Mismatches:  243  Query Match:  79.18%  10dels:  243  Query Match:  244  Query Match:  245  Query Match:  246  Query Match:  247  Query Match:  248  Query Match:  248  Query Match:  248  Query Match:  249  249  256  267  267  277  287  288  287  287  297  298  298	RESULT 11 AX365517 LOCUS DEFINITION Sequence 2 from Patent WOO208257. ACCESSION AX365517 VERSION AX365517 VERSION AX365517  VERSION AX365517  VERSION AX365517  AX365517  VERSION AX365517  INTERPRENCE 1 AUTHORS Interpretate West and uses thereoff TITLE How 1.2954  FEATURES SOUTCE BRISTOL-MYERS SOUTBE COMPANY (US) FEATURES SOUTCE 1.2954  BASE COUNT 715 a 869 c 780 g 590 t	Qy 436 ArgThrProLeuProProGlyAlaProSerProGluSerLysLysAsnGlnLysLysGln 455

B 8

Qy Db	рь Оу	Oy Db	Qy	P 84	Оу	ОУ	Оy	B 5	<u> </u>	Qy	pb Qy	Db	Qy	P 9	Оy	D Qy	Db Qy	B 2	₽ ₽	Qу	<b>;</b>
1149 GAGGGTCTGCACTGCAGCTGCTCCTCCCAGGCCAGCCCGGCCCCCTCTCTGCGCTGGTGG 1208 354 354 1209 CTTGGGGAGGAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGC 1268	1089 CTCAGCCTCCGGGCACTACTCCCCGAAGCTGCTGGGCCCCTCCTGCTCCTGGGAGGCT 1148	1029 GAGCACGAAGGAGAGTTCACCTGCCACGCTCGGCACCCACTGGGCTCCCCAGCACGTCTCT 1088  348 LeuSerLeuSerValH1sTyr	28 GluH1sGluGlyGluPheThrCysH1sAlaArgH1sProLeuGlySerGlnH1sValSer	308 ValLeuSerProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnVal 327 	288 LeuValCysValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGln 307 	268 ValleuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCys 287 	253ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr 267	729 TCAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGAC 788	9 TCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGAT	Ν	252 252 609 GCTGACAGCCAGCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCG 668	549 CAGGGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCT 608	52	238 ProArgAspLeuValIleSerIleSerArgAspAsnThrProAsp 252 	218 AspPheSerArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAla 237 	198 SerValLeuSerPheThrProArgProGlnAspH1sAspThrAspLeuThrCysH1sVal 217 	178 PheSerTrpThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPhe 197	371 371	63 AAAGTAACA	303 TTTCGGGTGGAGAGGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTTTCT	
Alignment Scores:  Pred. No.:  1.28e-105  Score:  1960.00  Matches:  Percent Similarity:  80.63%  Best Local Similarity:  80.21%  Mismatches:  2	/OD_XIELE LANCUS 70000 7701502CB1"  BASE COUNT 533 a 709 c 620 g 459 t  ORIGIN	source	- s o	Baugin, M.R., Lu, D.A., rue, Ramkumar, J., Lu, Y., Lo, T.P and Yao, M.G. Immunoglobulin superfamily	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho	_	AX497858  AX497858  LOCUS  AX497858  AX497858  ACCESSION  AXA07858  AXA07858	Db 1809 AGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTCCAA 1868	493 ArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLysPheGln	Oy         473 SerGlnGluSerGlnGluGluLeuHiSTyrAlaThrLeuAsnPheProGlyValArgPro 492		Db 1629 AACAGTCCTCGGACCCCTCTTCCACCAGGTGCTCCCCCAGAATCAAAGAAGAACAG 1688  Oy 453 LysLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAlaProGlu 472	433 AsnSerProArgThrProLeuProProGlyAlaProSerProGluSerLysLysAsnGln	Qy 413 IleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAlaThrPro 432	393 ArgThrGLHThrGLHThrProArgProArgPheSerArgHISSerThrLLELEHASPTYr	3/3 LIETTERALBEULFELFRELEUCYSLEUAIBLEUITE LIEMECLYSLIEUEUPFOLYSATG	355tystysG.tyteuileSerThrAlaPheSerAsnGtyAlaPheLeuGtyTleGty	1329 AGGCTCCGCTGTGAGGCCTGGAACGTCCATGGGGCCCAGAGTGGATCCATCC	Oy 354 354	354	-

Db !	OV B	Qy	Qу	Db	Qy Dy	Qу	Qу Db	Qу	Qу	Qу	Qу	Qy Db	δ δ	Oy Db	Qу	Qy		Query I DB:
4 TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTG 16	1484 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCCC 1543	252 252	252	1364 GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCTGACAGC 1423	241 LeuVallleSerIleSerArgAspAsnThrProAsp	221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240 	201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220 	181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200 	161 ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp 180 	141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 160 	121 GluargGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140 	01 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 12 	GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn	61 PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80 	41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60 	21 PheTrpIleArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 	1 MetLeuLeuProLeuLeuLeuSer 	Match: 72.43% Indels: 90 Gaps: 1 937-636-3 (1-512) x AX497858 (1-2321)
Qy 163 IleCysValPheAsnTrpAlaPheGluGluCysProProSerPheSerTrpThrGly 182	72 ACTCAGAAGCCTGATGTCTACATCCCCGAGACCCTGGAGCCCGGGCAGCCGGTGACGGTC	Db 12 GGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTTTCT	GlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThrAlaLeu 	6 Gaps: -937-636-3 (1-512) x AX365518 (1-2823)	ilar Simi	T 677 a	rce	Novel Siglecs and uses Patent: WO 0208257-A 3 BRISTOL-MYERS SQUIBB C	-	Κ	AX365518 AX365518 LOCUS AX365518 AX365518 AX365510		Qy 351 SerValHisTyrLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370	Qy 331 GlyGlubheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350	311 ProserGinProserAsperoGiyValLeuGinLeuProArgValGinValGinHisGiu	291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer	Qy       271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCys       290	Qy 253ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270

CTCCAGAGAACCTGAGATGATGGTTTCCCAAGCAAACAGGACAGTCCTGGAAAACCTTGGAAACCTTGGATGGTTTCCCAAGCAAACAGGACAGTCCTGGAAAACCTTTCGAAACCAGGACAGTCCTGGAAAACCTTTCGAAACCAGGACAGTCCTGGAAAACCTTTTTGGAACGGACGG	183 AlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeuSerPhe 202
LOCUS AX365544 LOCUS ACCESSION AX365544.1 GI:18697099  KEYMORDS SOURCE ORGANISM Synthetic construct ORGANISM Synthetic construct AUTHORS AUTHORS AUTHORS AUTHORS FEATURES SOURCE LOCUSTION AUTHORS FEATURES SOURCE SOURCE LOCUSTION BRISTOL-MYERS SOUIBB COMPANY (US) FEATURES  BRISTOL-MYERS SOUIBB COMPANY (US) FEATURES  LOCUSTION JOHN LEFT-TANN-30630° ADALTYPE-"Genomic DMA" //DL-XFEF-"TAXON:3630° ADALTYPE-"TAXON:3630° ADALTYPE-"TAXON:3630° BRISTOL-MYERS SOUIBB COMPANY (US) FEATURES  LOCUSTION JOHN LOCU	358 LeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThrAla

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Source	310 1328	291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 3 	Дb
TITLE NOVEL SIGNATURES NOVEL SIGNATURES BRISTOL-PERMITTEES	290 1268	271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCys 2	Qy
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SULT 15	1028	9 CAGCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCCCATCCC	рb
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Qy 422 LeuAla	180	61 ThrVall1eCysValPheAsnTrpAlaPheGluCluCysProProProSerPheSerTrp	Qγ
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1500	120	CysserLeuvalileArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal	2 5
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35.1	68	309 TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA 3	Ъ
Ωy 331 G1yG1u           Db 1389 GGAGAG	80	61 PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg (	Qy
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AUTHORS TITLE JOURNAL FEATURES sourc	RESULT 15 AX365519 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	Qy Db 1	Qy Db 1	Qγ Db 1	Qy Db 1	Qy Db	Qy Ωb 1	Qу	Qy	Qy	Qу	Qу Db	Qy Db 1	Qy Db 1
Longphre,M., Chang,H. and Whitney,G. Novel siglecs and uses thereof Patent: WO 0208257-A 4 31-JAN-2002; BRISTOL-MYERS SQUIBB COMPANY (US) Location/Qualifiers e 1. 1665 /mol_type="genomic DNA" /db_xref="taxon:9606"	AX365519  1665 bp DNA linear PAT 15-FEB-2002 Sequence 4 from Patent WO0208257.  AX365519  AX365519.1 GI:18697088  Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	507 aGluValLySPhe 511             937 TGAGGTCAAGTTC 1949	496GlnalaAspTyral 507 :::       :::     877 CATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGACGTGAGCCACGAAGACCC 1936	478 uGluLeuHisTyrAlaThrLeuAsnPheProGlyValArgProArgProGlu 495 :::	466 rSerThrGln	452 nLysLysGlnTyrGlnLeuProSerPheProGluProLysSe 466	441 ProGlyAlaProSerProGlu-SerLysLysAsnGl 452	422 LeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgThrProLeuPro 440	403 PheSerArgHisSerThrIleLeuAspTyrIleAsnValValProThrAlaGlyPro 421 ::::::	391 LysArgArgThrGlnThrGluThrProArgPro	371 IleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuPro 390	351 SerValHisTyrLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370	331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350 	311 ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGluHisGlu 330 

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AGGACCACAACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGC 541	CCCCAGGACCACAACACCGACCTCACC	82
SysHisValAspPheSerArgLysGlyValSer 225	-8	206
:rSerGlnGlyThrLysProThrThrSerHisPheSerValLeuSerPheThrProArg 205 	SerSerGlnGlyThrLysProThrThr	186 422
PheAsnTrpAlaPheGluGluCysProProProSerPheSerTrpThrGlyAlaAlaLeu 185 	PheAsnTrpAlaPheGluGluCysPrc                   TTTAACTGGGCCTTTGAGGAATGTCCA	166 362
<pre>sspValTyrIleProGluThrLeuGluProGlyGlnProValThrValIleCysVal 165                                     </pre>	ProAspValTyrIleProGluThrLeu                    CTGATGTCTACATCCCCGAGACCCTG	146 302
ArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLys	VelargTyrasnPheMetasnAspGly 	126 242
gAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgValGluArgGlySerTyr 125 	ArgAspAlaGlnMetGlnAspGluSer 	106 182
hrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsnCysSerLeuValIle 105 	ThrargGlyargPheGlnLeuThrGly	86 122
ThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArgGluValGluMetSer 85 	GluThrThrLysGlyAlaProValAla 	62 62
roArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrpPheLysAlaValThr 65 	ProArgGlnAspTrpThrGlySerThr             CCCGACAAGACTGGACAGGGTCTACC	2 46
5)	3 (1-512) x AX365519 (1-166	-09-937-636-
Length: 1665 Matches: 336 Conservative: 2 Mismatches: 2 Indels: 90 Gaps: 1	es: 3.07e-92 1728.00 rity: 78.60% ilarity: 78.14% 63.86%	Alignment Scor Pred. No.: Score: Percent Simila Best Local Sim Query Match: DB:
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Search completed: October 8, 2003, 21:48:29 Job time: 5749 secs

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and is derived by analysis of the total score distribution.

SUMMARIES

Result

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10	2265	83.7	2764	25	ABX98713	Novel human secret
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12	2265	83.7	2764	25	ABX92481	cDNA encoding huma
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31	1454.5	ü	2052	24	ABK43375	Siglec-BMS-L3a-hIg
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# ALIGNMENTS

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Key CDS	Homo sapiens.		obesity-relat	Human obesity		Human obesity		12-FEB-2001		AAA37847;		AAA37847 star	AAA37847	RESULT 1	
Location/Qualifiers 11536			obesity-related disorder; therapy; ds.	Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity;		Human obesity protein binding protein-2 homologue coding sequence #1.	•	(first entry)				AAA37847 standard; DNA; 1536 BP.			
				<pre>homologue;</pre>		? homologue					< =	<b>Y</b>	_		i
				hOB-BP2h; obesity		coding sequence #1				•	-	2	20110	1) A TOX	

Pred. score

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed,

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                                                                                                                                                                                                                                                                                                                   This sequence encodes a human obesity protein binding protein-2 homologue (hoB-BP2h) of the invention. The hoB-BP2h nucleic acids and polypeptides may be used for the manufacture of a medicament for the treatment of obesity and/or obesity-related disorders. The hoB-BP2h nucleic acids are useful as probes or amplification primers in the detection, quantification or isolation of gene sequences or treascripts, for recombinant expression of hoB-BP2h polypeptides, as immunogens in the preparation and screening of antibodies, and in sense or antisense suppression of one or more hoB-BP2h genes or nucleic acids, host cell or tissue in vivo or in vitro. Antigenic epitope-bearing peptides and polypeptides are useful for raising or screening antibodies that specifically binds to the hoB-BP2h polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human obesity protein binding protein-2 homologue nucleic aci polynucleotides and polypeptides useful for producing medicament treating obesity and/or obesity-related disorders -
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                CysSerLeuValIleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal
                                                                         PheLysalaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg
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                                                  ThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThrAlaLeuLeuPheLeuCys
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 Alignment Scores Pred. No.:
                                                                               CC related lectin) protein (I). Pharmaceutical compositions comprising (I) CC are useful for treating immune system diseases such as asthma, leukaemia CC or other allergic or inflammatory diseases. Extracellular domains of (I) CC represent potential markers for screening, diagnosis, prognosis, CC follow-up assays, and imaging methods. (I) is useful as a target for CC drugs which inhibit inflammation, tissue damage and remodeling in CC asthma, and inflammatory diseases such as allergic rhinitis, CC osteoarthritis, Crohn's disease, psoriasis, rhemmatoid arthritis, CC onjunctivitis, etc. (I) is also useful for monitoring the course of CC disease or disorders, and for identifying agents that bind with and/or CC modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid CC molecules (II) encoding (I) are useful in diagnosis and/or prognosis CC nucleotide sequences and/or SIGLEC-BMS proteins in a biological sample. (I) are useful as nucleic acid probes are useful for screening genomic Clibrary to isolate a genomic clone of SIGLEC-BMS gene copy number is determined for detecting diseases or disorders associated with SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also cused to detect, sort or isolate cells expressing SIGLEC-BMS proteins and in diagnostic imaging technology. ABK43360-ABK43411 represent transcripts or collate cells expressing SIGLEC-BMS proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukaemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's dise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma; immune system disease; leukaemia; allergy; inflammatory disease; tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease; psoriasis; rheumatoid arthritis; conjunctivitis; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding sialic acid-binding Ig-related lectin,
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or other allergic or inflammatory diseases. Extracellular domains of (I) CC represent potential markers for screening, diagnosis, prognosis, CC follow-up assays, and imaging methods. (I) is useful as a target for CC drugs which inhibit inflammation, tissue damage and remodeling in CC asthma; and inflammatory diseases such as allergic rhinitis, Crohn's disease such as allergic rhinitis, CC osteoarthritis, etc. (I) is also useful for monitoring the course of CC disease or disorders, and for identifying agents that bind with and/or CC modellate the biological activity of SIGLEC-BMS proteins. The nucleic acid CC molecules (II) encoding (I) are useful in diagnosis and/or prognosis CC mucleotide sequences and/or SIGLEC-BMS proteins in a biological sample. CC (II) are useful as nucleic acid probes are useful for screening genomic CC library to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS gene copy comber is determined for detecting diseases or disorders associated with CS IGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells expressing SIGLEC-BMS proteins and in diagnostic imaging technology. ABK43360-ABK43411 represent The invention relates to an isolated SIGLEC (stalic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising (I) are useful for treating immune system diseases such as asthma, leukaemia or other allergic or inflammatory diseases. Extracellular domains of (I) acid

Sequence BP; 699 A; 933 Ç 790 ç; 602 T; 0 other;

Query Match:	Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:
95.36%	73.17%	73.31%	2580.50	5.94e-176	
Indels:	Mismatches:	Conservative:	Matches:	Length:	
185	1	Ļ	510	3024	

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3ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270	1089 TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGGGCCCTGGACCTCTCTGTG 1148	252 252	1029 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGGATTCAGGGCGC 1088	252 252	969 CAGCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCCTCCTCGTCCCATCCC 1028	252 252	909 GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCTGACAGC 968	252 252	849 CTTGTTATCAGCATTTCACGTGACAACACGCCAGCCCTGGAGCCCCAGCCCCAGGGAAAT 908	241 LeuVallleSerIleSerArgAspAsnThrProAsp 252	221 ArgLysdlyValSsrAlaGlnArgThrValArgLeuArgValAlaTyrAlaEroArgAsp 240	29	201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220	69 ACGGGGGCTGCCCTCTCCCAAGGAACCAACGACCTCCCACTTCTCAGTGCTC 7	81 ThrGlvAlaAlaLeuSerSerGlnGlvThrLvgDroThrThrSerHisPheSerValLeu 20	161 ThrVallleCysValPhaAsnTrpAlaPhaGluGluCysProProProSerPhaSerTrp 180 	ייי פיירבומערורעמעטטררנומעומורנוערטיררמעטערררנומעטערררנומעטררררמעטערררטע	141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 160 	68	121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140	429 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 488	101 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 120	369 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC 428	81 GluvalGlumetSerThrargGlyargPheGlnLeuThrGlyAspProAlaLysGlyAsn 100		61 PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg	9 TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG 3	4] CysSerDheSerTyrProArgGlnAsgTrpThrGlySerThrProAlaTyrGlyTyrTrn 60	21	ATGUTAUTGUCAUTGUTGTEUTCGUTGCTGGGUGGGGGTATGG	1 MetLeuLeuProLeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20	37-636-3 (1-512) x ABK43373 (1-3024)	24 Gaps: 2
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                                                                                                                                                                                                                                                                                                                                                                              related lectin) protein (1). Pharmaceutical are useful for treating immune system diseas or other allergic or inflammatory diseases.
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DB; AAU87074.
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system disease; leukaemia; allergy; inflammatory disease;
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rgic or inflammatory diseases. Extracellular domains of
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                                       CAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTCCTGGAA
                                                                                                                                                                               CAGCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCCCATCCC
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                                                                                   TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTG
                                                                                                                                  TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC
                                                   -ProproGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu
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RESULT 5 AAZ34109 ID AAZ3 XX AC AAZ XX DT 07-E XX Hume		Db
AAZ34109 standard; cDNA; 2764 BP.  AAZ34109;  07-DEC-1999 (first entry)  Human PRO940 nucleotide sequence.  Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein; ss.  Homo sapiens.  W09946281-A2.  16-SEP-1999; 99WO-US05028.  10-MAR-1998; 98US-0077450.	431 1515 451 1575 471 1635 491 1695 511	291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValleuSer 310
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Local Similarity:
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RESULT 6
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XXX Huma
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Kljavin
Shelton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel PRO polypeptides and polynucleotides to target bloactive molecules to specific cellular activities -
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Kuo SS, Nap
Stewart TA,
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PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA;
TA, Tumas D, Williams PM, Wood WI;
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PRO polypeptide: mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; col adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disord
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                                                                                                                                 ProGluSerGlnGluSerGlnGluGluLeuHisTyrAlaThrLeuAsnPheProGlyVal
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                                          PheGln 512
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  16-SEP-1998;
07-OCT-1998;
01-DEC-1998;
08-MAR-1999;
                                                                                                                                                                                    Human; secreted protein; transmembrane protein; cytostatic; gene Therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour;
                                                                                                                                                                                                                                                                         20-MAY-2003
                                                                   02-JUL-2002;
                                                                                                                     US2003036157-A1
                                                                                                                                                                        gene;
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CY - G AG T T T T T T T T T T T T T T T T T	
A65.00  Antches: 4.75%  A.75%  Mismatches: 3.70%  ABX98713 (1-2764)  Conservative: Gaps:  ABX98713 (1-2764)  ACTGCTGCTGCTGCTGCTGGGCGGGTGCTGCTGCTGCTGCT	Length:
Matches: 450 Conservative: 1 Mismatches: 3 Indels: 148 Gaps: 2 1-2764) 1-2764) 1-2764) 1-2764) 1-2764) 1-2764 1-27	
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832 TACACC 253 892 CAGTAN 271 ASNLE               952 AACCTN 291 ValTh 1012 GTCAC 311 ProSet               1072 CCCTCC 331 GlyGlt             1132 GGAGAA 351 Serval             1132 TCCGTC 371 IleGlt             1192 TCCGTC 371 IleGlt             1192 TCCGTC 391 LySAr               1192 TAGAGA 431 ThrPr 431 ThrPr 431 ThrPr	465 181 ThrGly 466 201 SerPhe 472 AGCTTC 221 ArgLys 1      532 AGAAAC 241 LeuVal 592 CTTGTT 252 652 GTCCCA 252 712 CAGCCC 252 772 TGGGGG
ProproGluAs	AlaAlaLeuSe
TACACCTGCCGAGCGGAGAACAGGCTTGCCTCCCAGCAGCCAGC	ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu
GTTCCCAGCAGC StValSerGlap	IrLysProThrT
GAAGCCCTGGAC	hrSerHisPhe
CTCTCTGTG 891 ValLeuGlu 270	SerValLeu 200

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RESULT 11

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2000WO-US13705

2000WO-US14941

2000WO-US15264

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2000WO-US23328

2000WO-US3328578

2000WO-US34956

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2000WO-US04341.
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99WO-US05028.
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29-AUG-2001;
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07-CCT-1998;
07-DEC-1998;
03-MAR-1999;
14-MAY-1999;
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25-AUG-1999;
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2001US-0854208.
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Pan Baker ΚP, P, Chen J, Smith V, W , Desnoyers L, Goddard A, Go Watanabe CK, Wood WI, Zhang Godowski PJ, ang Z; Gurney AL

2003-332039/31. DB; ABU67464.

New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification -

Claim 2; Fig 117; 706pp; English.

CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that CC specifically binds to the PRO polypeptide, a method for stimulating the CC contacting the blood a PRO polypeptide, a method for stimulating the CC contacting the blood a PRO polypeptide, a method for stimulating the CC contacting the blood a PRO polypeptide, a method for stimulating the CC cells with a PRO polypeptide, a method for detecting the presence of a CC tumour in a mammal and an oligonucleotide sequences are useful as probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy CC (e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight markers for protein electrophoresis purposes, for chromosome identification, as chromosome markers, as therapeutic agents, for stimulating the release of TNF-alpha from human blood, for Stimulating the presence of a tumour. The PRO polypeptides and uncleic cacids may also be used diagnostically for tissue typing. The sequences CC presented in ACA05700-ACA06004 are the CDNAs encoding the PRO invention discloses human nucleic acids encoding secreted g secreted and an antibody that

689 A. 798  $\Omega$ 717 છ 560 Τ, 0 other;

Pred. No.: Score: Alignment Scores: Percent Similarity: 2.54e-153 2265.00 74.92% Length: Matches: Conservative:

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                                                                           CAGCCCCCTGCCACACTGAGCTGGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCCCATCCC
                                                                                                                                                                 LeuValIleSerIleSerArgAspAsnThrProAsp---
                                                                                                                                                                                                      ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp
                                                                                                                                                                                                                                                                                         {\tt ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu}
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                                     TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCCGGGGTGAAGGCTGGGGATTCAGGGCGC
                                                                                                                 GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCTGACAGC
                                                                                                                                                      CTTGTTATCAGCATTTCACGTGACAACACGCCCAGCCCTGGAGCCCCCAGCCCCAGGGAAAT
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RESULT 12
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      Human; PRO polypeptide; secreted and transmembrane protein; immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia; cardiac insufficiency; nervous system disorder; kidney disorder; bone disorder; cartilage disorder; arthritis; tumour; wound healing; genetic disorder; cytostatic; antidiabetic; antiinflammatory;
                                                                                                        ABX92481;
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2000WO-US03565
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2000WO-US15264
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9705-065311P.
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9805-077-632P.
9805-077-649P.
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9805-078910P.
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97US-064249P.
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S-079923P.
S-0267213.
S-0040220.
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26-JUN-1998;
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02-NOV-1998;
06-NOV-1998;
07-DEC-1998;
07-DEC-1999;
10-MAR-1999;
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12-APR-1999;
14-MAY-1999;
25-AUG-1999;
25-AUG-1999;
08-NOV-2000;
27-NOV-2000;
27-NOV-2000;
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27-MAR-2001;
110-MAY-2001;
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99US-0380138

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2000US-07709238

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98US-0168978.
98US-0184216.
98US-0187368.
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Ashkenazi A, Ferrara N, Goddard A, Kljavin IJ, Shelton DL, Ą A, Baker KP, I Filvaroff E, Godowski PJ, , Kuo SS, Napi , Stewart TA, Napier MA, I IA, Tumas D, Botstein D, Desnoyers L, Eaton D; Fong S, Gao W, Gerber H, Gerritsen Grimaldi JC, Gurney AL, Hillan KJ; pier MA, Pan J, Paoni NF, Roy MA; Tumas D, Williams PM, Wood WI; ME;

WPI; 200 P-PSDB; 2003-288163/28. DB; ABU61110.

Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies .

Claim 2; Fig 92; 459pp; English.

The present invention relates to the isolation of novel human PRO CC polypeptides, and the polynucleotide sequences encoding them. The CC PRO polypeptides are useful for detecting other PRO polypeptides, for CC linking bioactive molecules to cells expressing PRO polypeptides, for CC linking bioactive molecules to cells expressing PRO polypeptides, CC for modulating biological activities of cells expressing PRO polypeptides, CC polypeptides, and for for identifying agonists or antagonists. The CC bioactive molecule maybe a toxin, radiolabel or antiopody, and causes CC apoptosis or death of the cell. The PRO polypeptides are useful for CC treating immune disorders, diabetes or hyper or hyporinsulinaemia, CC bone and cartilage disorders or arthritis, tumours, and wound healing. CC the polypuclectide sequences encoding PRO polypeptides are useful as CC hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for CC generating transgenic animals or knockout animals, for the genetic CC analysis of individuals with genetic disorders, and in gene therapy. CC The present sequence data for this patent was obtained in electronic CC format directly from the USPTO web site at CC sequence data for this patent was obtained in electronic CC sequence and the USPTO web site at

Sequence 2764 B₽; P. 798 Ç g; 560 .. 0 other;

			Score:		Alignment Scores:
83.70%	74.75%	74.92%	2265.00	2.54e-153	
Indels:	Mismatches:	Conservative:	Matches:	Length:	
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                                                  TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC
                                                                                 CAGCCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCCTCCTCCTCCCATCCC
                                                                                                                  GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCTGACAGC
                                                                                                                                                                                           ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp
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RESULT 13
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protein electrophoresis; tum
chondrocyte differentiation;
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                                       ss; cytostatic; chromos
oresis; tumour necrosis
rentiation; chondrocyte
                                                                                                                          cDNA;
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                                       chromosome mapping; gene mapping;
ecrosis factor-alpha; TNF-alpha; blood;
drocyte proliferation; tumour.
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Qy 61 PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80	Qy 21 PheTrplleArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40	09-937-636-3 (1-512) x ABX97802 (1-2764)  1 MetLeuLeuProLeuLeuLeuSerSerLeuLeuGlyGlyS	ignment Scores: ed. No.: ore: scent Similarity: ccent Similarity: ery Match:	02-SEP-1998; 98US-098821 02-SEP-1998; 98US-098821 02-SEP-1998; 98US-099802 09-SEP-1998; 98US-099762 10-SEP-1998; 98US-099754 10-SEP-1998; 98US-099754 10-SEP-1998; 98US-099763 10-SEP-1998; 98US-099763	18-AUG 1998; 98US-096599 18-AUG-1998; 98US-097022 26-AUG-1998; 98US-097952 26-AUG-1998; 98US-097954 26-AUG-1998; 98US-097954 26-AUG-1998; 98US-097971 26-AUG-1998; 98US-097971 26-AUG-1998; 98US-097974 01-SEP-1998; 98US-098016 01-SEP-1998; 98US-098016	PR 26-JUN-1998; 98US-090862P. PR 26-JUN-1998; 98US-090863P. PR 26-JUN-1998; 98US-091010P. PR 17-JUL-1998; 98US-09135P. PR 01-JUL-1998; 98US-091478P. PR 02-JUL-1998; 98US-091426P. PR 02-JUL-1998; 98US-091226P. PR 02-JUL-1998; 98US-091628P. PR 02-JUL-1998; 98US-091628P. PR 02-JUL-1998; 98US-09162P. PR 10-AUG-1998; 98US-095282P. PR 10-AUG-1998; 98US-095282P. PR 11-AUG-1998; 98US-09575P. PR 17-AUG-1998; 98US-096757P. PR 17-AUG-1998; 98US-096757P. PR 17-AUG-1998; 98US-096757P. PR 17-AUG-1998; 98US-096757P. PR 17-AUG-1998; 98US-096891P. PR 17-AUG-1998; 98US-096891P. PR 17-AUG-1998; 98US-096891P.
1132 GGAGAGTTCACCTGCCACGCTCCGCACCCACTGGGCTCCCAGCACGCCTCCTCAGCCTCC  351 SerValHisTyrLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly	Qy 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgClyGlnValLeuSer 310	892 CAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCCAAGCAAACAGGACAGTCCTGGAA 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCys	TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC TACACCTGCCGAGCGAGACAGGCTTGGCTCCCAGCAGCCAGC	GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGGCTCCTCTGTGCTGCTGACAGC 7	Qy 221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240	Qy       121 GluargGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140         Db       406 GAGAGAGGAAGCTATGGACATATAATTTCATGAACGATGGGTTCTTTCT

30-NOV-1999; 99WO-US28301 01-DEC-1999; 99WO-US28301 30-DEC-1999; 99WO-US28551 30-DEC-1999; 99WO-US31274. 05-JAN-2000; 2000WO-US00219. 18-FEB-2000; 2000WO-US003141. 18-FEB-2000; 2000WO-US04342. 22-FEB-2000; 2000WO-US04341. 01-MAR-2000; 2000WO-US05004. 01-MAR-2000; 2000WO-US05601. 02-MAR-2000; 2000WO-US05601. 10-MAR-2000; 2000WO-US05684. 11-MAR-2000; 2000WO-US05884. 13-MAR-2000; 2000WO-US05884. 15-MAR-2000; 2000WO-US05884. 17-MAR-2000; 2000WO-US05884.	16-SEP-1998; 98WO-US13330. 07-OCT-1998; 98WO-US21141. 01-DEC-1998; 98WO-US25108. 08-MAR-1999; 99WO-US05028. 10-MAR-1999; 99WO-US05190. 14-MAY-1999; 99WO-US10733. 02-JUN-1999; 99WO-US10733. 01-SEP-1999; 99WO-US21011. 15-SEP-1999; 99WO-US21090.	Homo sapiens. US2003027272-A1. 06-FEB-2003. 21-JUN-2002; 2002US-0176492.	SULT 14 X78586 X78586 X78586; ABX78586;  15-APR-2003 (first entry) Human PRO polynucleotide #59. Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach; liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT; antibody-dependent enzyme mediated prodrug therapy.	ASPTYTILEASNVBILLINGACCCCAGGGCCCCCAGGTCCCCGCACAGCACCAGGCCCCGCGCAGGCCCCGCGCACAGCACCAGGCCCCGCGCCCCGCGCCCCGCGCACAGCCGCAACCAGCCCCAGGCCGCAACCAGCCGCAACCCGCAACCCGCAACCCGCAACCCGCAACCCGCAACCCCAGACCCCCC	
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                                                                                                                                                    {\tt ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProSerPheSerTrp}
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Matches:
Conservative:
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Search completed: October 8, 2003, 20:13:22 Job time : 459 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

RESULT 1 AK042488 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM AK042488

2017 bp mRNA linear HTC 05-DEC-2002 Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630096C01 product:weakly similar to SIALIC ACID-BINDING LECTIN [Homo sapiens], full insert sequence.

AK042488

Mus musculus (house mouse) AK042488.1 GI:26335142 HTC; CAP trapper. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

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REFERENCE
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2017)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                             Submitted (16-JUL-2001) Yoshihide Hayashizaki, The
                                                                                                          Direct Submission
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                                                               273
                                                                                                                                                                           213 TTCCTACAGGTGCAGAGAATTGTGAAGGCACAGGAGGGTCTGTGCATCTTCGTGCCCTGC
     62
                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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URL:http://fantom.gsc.riken.go.jp/.
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Please visit our web site for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
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  LysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArgGlu
                                                                                         SerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrpPhe 61
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/db_xref="G1:26335143"
/db_xref="G1:26335143"
/translation="MSLLIFILSFLLDGPQGQMESYFLQVQRIVKAQEGLCIFVPCSF
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SLLIKDVQWGDSTNYFFRMERGFERFSFKEEFRLQVBALTQKPDIFIFBVLEFGEPVT
SLLIKDVQWGDSTNYFFRMERGFERFSFKEEFRLQVBALTQKPDIFIFBVLEFGEPVT
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="3 days neonate"
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/strain="C57BL/6J"
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Bp 191 91006 EVRY codex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9384.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq-CSOAIO25BB12QP1&cluster=9384.r. Contact: Feng Liang Email : fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOAIO25BB12QP1.  Fengures Location/Qualifiers source /organism="Homo sapiens"	SOURCE Homo sapiens (human)  SOURCE Homo sapiens  ORGANISM Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REPERENCE 1 (bases 1 to 1201)  AUTHORS L1,W.B., Gruber,C., Jessee,J. and Polayes,D.  TITLE Full-length cDNA libraries and normalization  JOURNAL Unpublished  CONMENT Genoscope - Centre National de Sequencage	SULT 2 345667 BX345667 BX345667 FINITION BX345667 Clone CSODIO25YC24 5- CESSION BX345667.1 GI:303730	Qy 421 ProLeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgThrProLeuPro 440	Db 1761 ACAGCATTCTCCAAGGGAGCAGTTTTGGCTTTGGCATCACAGCCTCCTTGCCCTTGTC 1820  Qy 381 LeualaLeuileileMetLysileLeuProLysArgArgThrGlnT	AACAGCTCCCTGAGCCTCCTTCAGGAGCTGGGGCCCAGCCTCTGGCTCAGCTGTGAGTCC	Db 1521 TGCTCCTCCAGAGCCTGGCCTGCCCTCCCTGCGGTGGGGGGGG	Db 1401 ACCTGTGCACAGAACCCACTGGGTGCCCAGCGCATCTCTCTGAGCCCTCTCTGTGCAC 1460  Qy 354 Tyr

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                        pLeuValIleSerIleSerArgAspAsnThrProAspProProGluAsnLeuArgValMe
                                                              rArgLySG1yValSerAlaG1nArgThrValArgLeuArgValAlaTyrAlaProArgAs
                                                                                                                uSerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSe
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/db_xref="taxon:9606"
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
/note="ist strand cDNA was primed, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
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	AUTHORS	JOURNAL MEDLINE PUBMED	TITLE		REFERENCE AUTHORS	JOURNAL MEDLINE PUBMED	TITLE	AUTHORS	JOURNAL MEDLINE PUBMED	AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	ACCESSION	RESULT 3 AK036698 LOCUS DEFINITION	Db 9	Оу	Db 8	0у 2	B dd	Qy 2
(., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, C., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Iann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Nush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Il, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Nordone Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Ushizaki, Y., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, Ishizaki, Y.	4 Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa.T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,	Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861	Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Yokazaki,Y., Muzamatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system384 format sequence pipeline with 384 multicapillary sequencer	Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaduchi, S., Ikedami, T., Kashiwadi, K.,	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,		in   -   -   -   -   -   -   -   -   -	2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Ttoh M., Konno,H., Okazaki,Y., Muramatsu.M. and Havashizaki.Y.	Meth. Enzymol. 303, 19-44 (1999) 99279253 10349636	Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning	AK036698.1 GI:26331615 HTC; CAP trapper. Mus musculus (house mouse) Mus musculus	rary, clone:9830164H23 product: D-BINDING LECTIN [Homo sapiens 36698	lín ull-	51	300 uSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnPro 314	891 TCAGAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCTGACAGCCAGC	280 lLeuGluGlyGlnSerLeuCysLeuValCysValThrHisSerSerProProAlaArgLe 300	850TCAGCCCTGGAACTCCAGGGAAACGTCATATATCTGGAAGT 890	AsnLeu

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Nature 409
21085660
11217851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Group Phase I & II Team.
Analysis of the mouse transcriptome based on of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3939)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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Please visit our web site for further
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SLLIKDVQWGDSTNYFFRWERGFERFSFKEEFRLQVEALTQKPDIFIFEYLEPGEPVT
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                                                                                                                                                                                                                                                                                                                           /note="unnamed protein product; putative
weakly similar to SIALIC ACID-BINDING LECTIN [Homo
saptens] (SPTR Q96RL6, evidence: FASTY, 61.6%ID,
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358	1892 TACGTTGGTCTCCTGGGGTCTTATAGGGCCGGTCCATTCCTTTTTGGGAAAATGAAAAGTC 1951	ਰ
2972 CAACTGCTCCTCCAGAGCCTGGCCTGCCCCTCCCTGCGCTGGCGGCTGGGGGAG		Ϋ́
357	1833 CTTCTCCCAGATGCCCCCAGATCTCTTGCTATCAGCATTTTCCATGACAATGT-ATCAGG 1891	ŏ
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201	1533 TGAGTTCAATGAAAGACCCTGCCTTAAACAATGTAGACAGTGATTCAGGAAGGTACC 1592	ŏ
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376	1473 GAGACAAGTGATCCCCCAAGGCAAGTGAGCTAGCTAGACTGGCTACCCCAATTAGCAAGCTC 1532	ō
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N	1293 AGTGAGTGCCAGGTCAGCCAGGGCTACACAGAGAAAACCCCTGTCTCAAAAAAAA	ŏ
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2312 GITCAGCAAGGCCAGICICITICGCCICCICIAIACIGCIGACAGCCAGCCCACTGCIACIACIGC	1233 CCAGCACTTGGGAGGAAGAGGCCAGGCGAATTTCTGAGTTTGAGGCCATCCTGGTCTACAG 1292	ō
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) h	1173 ATGAGTAGGCTGATAAAGAGTTTGACACACAGCCAGGCGCGGTGGTGCACACCTTTAGTC 1232	ŏ
Th 3252 CTCTTCTCTCTCTCTCTCTTCTAGTCTCTAGAGAGTGAGAGAATCCTTCAGAAA	236 236	Ÿ
25.1	1113 AACATATATACATGATAGAATCCATGATCTTGTATAAATGGAGCAAAGGTTGCTGGGGGAG 1172	ŏ
Db 2192 TCTCATTTTTGTCTGTTTCTCTCTTCATTCTTTTTCTCTCTATCACTGTCCATCTCATCCT		

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BASE COUNT
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AUTHORS
TITLE
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1 (bases 1 to 1099)
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Tissue Procurement: Invitrogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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                                             225
                                        /note="Organ: Ovary (Dool of 3); Vector: pCMV-SPORT6;
Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

a 360 c 283 g 230 t 1 others
                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                             /clone_lib-"NIH_MGC_125"
                                                                                                                                                                                                              /clone="IMAGE:5587803"
/lab_host="DH108"
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              CAGCCCCCCTGCCCCGTTGAGCTTGGGTTCCTGCCAGGCAAAAAGTTCCTTCTCCTCCGA
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
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ValLeuGluGlyGlnSerLeuCysLeuValCysValThrHisSerSerProProAlaArg
                                             MetValSerGlnAlaAsnArgThrValLeuGluAsnLeuGlyAsnGlyThrSerLeuPro
                             ATGGTTTCCCAAGCAAACAGGACAGTCCTGGAAAACCTTGGGAACGGCACGTCTCCCCA
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quality sequence stop: 685.
Location/Qualifiers
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                                                                                                                                                                                                                                                        /note="Organ: Spleen; Vector: pOTB7; Site_1: XhoI; Site_2 EcoRI; cDNA made by oligo-dT priming. Directionally clone into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a 304 c 244 g 151 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6215765"
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                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Cercopithe
                                                                                                                                   Macaca mulatta (rhesus monkey)
Macaca mulatta
                                                                                                                                                                                              MMSP0040_D05 MMSP Macaca
CB554607
 Contact: Holzman
                            Expressed sequence
                                                      Katze, M.G., Bumgarner, R.,
                                                                       Cercopithecinae; Macaca.
1 (bases 1 to 667)
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cDNA, mRNA sequence
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                                                        Amjadi, M.
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University of Washington
Box 358070, Seattle, WA 99
Tel: 206 732 6156
Fax: 206 732 6055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ted@locke.hs.washington.edu
Similar to GenBank entry AF311905 AF311905
acid-binding Ig-like lectin 10 (SIGLEC10) m
8/2001
Plate: MMSP0040 ~~~~~~
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/mol_type="mRNA"
/db_xref="taxon:9544"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone from S. Wiemann, Molecular Genome Analysis, German Candersearch Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Center for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.

No Sl sequence available.
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ann S.;
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/mol_type="mRNA"
/mol_type="mRNA"
/organism="Homo sapiens"
/clone="DKFZP779N169"
/clone=lib="779 (synonym: hnccl). Workers of the Sfila + Sfila 
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AUTHORS
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5587773"
/lab_host="DH10B"
                                                                                                                                         /note="Organ: Ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: ECORV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036. "
                                                                                                                                                                                                                                                                                  /clone_lib="NIH_MGC_125"
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                                                        CAGCCTTCCTGCACCTTCCCGGCGGTTGGGTCCCTCCCCTCATGTAGTAAATCTCCCCCAC
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                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution information can
found through the I.M.A.G.E..Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                      Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                               {\tt AsnThrProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrVall}
                                                                                                                                                                                                                                         ThrValArgLeuArgValAlaTyrAlaProArgAspLeuValIleSerIleSerArgAsp 248
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/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
/note="Organ: pooled lung and spleen; RNA source
site_1: Not1; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
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4
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Iton,M., Iton,M.
                                                                                                                                                                                                                                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system --384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cdarninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new of Genome Res. 10 (10), 1617-1630 (2000)
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2478 bp mRNA linear HTC 05-DEC-2002 Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:E230037K16 product:SIALIC ACID-BINDING LECTIN SIGLEC-F homolog [Mus musculus], full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci, P. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGA 731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValSerLeuSerLeuSerValHisTyrLysLysGlyLeuIleSerThrAlaPheSerAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValCys-----ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArg
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Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagaoka,S., Sasaki,N., Carninci,P.,
Kitsunai,T., Tashiro,H., Itoh,M.,
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramotto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Numazaki, A., Murata, M., Koya, S., Kurihara, C., Matsuyama, T., Numazaki, R., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Naramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2478)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA library was prepared and sequenced in Mouse Encyclopedia Project of Genome Exploration Resear Genomic Sciences Center and Genome Science Labora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                    /note="unnamed protein product; SIGLEC-F homolog [Mus musculus] FASTY, 95.9%ID, 100%length, matc
                                                                                                                                                                                                                                                                                               429.
                                                                          putative"
/codon_start=1
/protein_id="BAC39955.1"
/db_xref="GI:26352650"
                                                                                                                                                                                                                                                                                                                     /tissue_type="oviduct"
/clone_lib="RIKEN full-length enriched mouse
/clore_tstage="2 days pregnant adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="FANTOM_DB:E230037K16"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="E230037K16"
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                                                                                                                                                            rct; SIALIC ACID-BINDING LECTIN
lus] (SPTR|Q920G3, evidence:
match=1770)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Research Group
Laboratory in R
                                                                                                                                                                                                                                                                                                                                                                     cDNA library'
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translation="MGKENSHNCSLDIRDAQKIDTGTYFFRLDGSVKYSFQKSMLSVL"/

ThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHisAspThrAsp 2	Qy 153 ThrLeuGluProGlyGlnProValThrValIleCysValPheAsnTrpAlaPheGluGlu 172	429 ATGGGAAGGAAAATAGTCATAAATTGCTCCCTGGACATCAGAGATGCACAGAAAATCGAC  113 GluSerGlnTyrPhePheArgValGluArgGlySerTyrValArgTyrAsnPheMetAsn	Oy  53 SerThrProAlaTyrGlyTyrTrpPheLysAlaValThrGluThrThrLysGlyAlaPro 72  54 Joy AAAGGTCCTGTCTTTGGCTACTGGTTCCGGGAGGGGCCAATATATTCAGCGGCTCCTCCA 368  55 Oy  56 Oy  57 ValAlaThrAsnH1sGlnSerArgGluValGluMetSerThrArgGlyArgPheGlnLeu 92  56 JIIIIIII	13 204 33 261	Pred. No.: 1.21e-45 Length: 2478 Score: 669.50 Matches: 187 Percent Similarity: 43.37% Conservative: 78 Best Local Similarity: 30.61% Mismatches: 176 Query Match: 24.74% Indels: 170 DB: 11 Gaps: 17 US-09-937-636-3 (1-512) x AK087658 (1-2478)	A_site
Qy 450 LysasnGlnLysLysGlnTyrGlnLeuProSer-PheProGluProLysSerSerTh 468	Qy 410 LeuAspTyrIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLys 429 ::	Db 1443 TCACAGGCAGCAAATCAGAAACCAGTAGAGGAACGGTCCTGGGGGCCATCTGGGGAGCT 1502  Qy 372 GlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeu 389		1203 AGCTGCTCCAGAGCCTGCCCTGCCCTCCCTGCCGTGCGGGGGGGG	Qy 333 PheThrCysHisAlaArgHisProLeuGlySergInHisValSerLeuSerLeuSerVal 352 :::	Db 852CCACAGAAGATGACCATCAGGGTGTCCTGGGGAAGTGACCAGGAACTAAAGTCCTG 908  Qy 273 GlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCysValThr 292    Oy 273 GlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCysValThr 292    Oy 274 GlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCysValThr 292    Oy 275 GlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCysValThr 292    Oy 276 GlyAsnGlyThrSerLeuProValLeuGluGlyGlnValLeuSerProSer 312    Oy 277 GlyAsnGlyThrSerLeuSerTrpThrGlnArgGlnValLeuSerProSer 312    Oy 278 HisserSerProProAlaargLeuSerTrpThrGlnArgGlnValLeuSerProSer 312    Oy 278 HisserSerProProAlaargLeuSerTrpThrGlnArgGlnValLeuSerProSer 312    Oy 278 GlyAsnGlyThll

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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onna Library Preparation: Life Technologies, Inc.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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Tissue Procurement: Life Technologies,
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 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 160
                                                         GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140
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/tissue_type="leukocyte"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12798 row: d column: 15
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates;
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/organism="Homo sapiens'
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/note="Vector: pcMv-SPORT6; Site_1: pcMv-SPORT6
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 997)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 725
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://image.llnl.gov
Plate: LLAM12789 row: f column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5', mRNA sequence.
BM921873
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                                                                               Gruber (Invitrogen). Research Genetics tracking 021. Note: this is a NIH_MGC Library." 314 c 266 g 201 t 1 others
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/mol_type="mRNA"
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                                TCCCCCTGCCAGGCTGAGCTGGGAACCCCGGAGGAATCTGACCCCTGTACCCCTCACAGGCC
                                                             rProProAlaArgLeuSerTrp--ThrGlnArgGlyGlnValLeuSerProSerGln-Pr
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                                                                                                                                        72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and advice from Piero Carninoi (RIREN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: NDAM363 row: g column: 23
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NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Institutes of Health, Mammalian
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AspGluSerGlnTyrPhePheArgValGluArgGlySerTyrValArgTyrAsnPheMet 131
                                                                                                           CCAGTGGCCACAAACGACCCAGACGAAGAAGTGCAGGAGGAGACCCGGGGCCGATTCCAC
                                                                                                                           ProValAlaThrAsnHisGlnSerArgGluValGluMetSerThrArgGlyArgPheGln
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                                                                  LeuThrGlyAspProAlaLysGlyAsnCysSerLeuValIleArgAspAlaGlnMetGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30337798"
/tissue_type="pre-eclamptic p
/lab_host="DB10B_TonA"
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Search completed: October 8, 2003, 22:41:04 Job time : 3195 secs

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Perfect score:
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1: /cgn2_6/ptodata/)

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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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US-08-468-859A-3

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STATE: F
COUNTRY:
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## ALIGNMENTS

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Sequence 3, Application US/09038832
Patent No. 6146845
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: (SAF-2)
TITLE OF INVENTION: (SAF-2)
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRSTESD for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/038,832
FILING DATE: 11-MAR-1998
CLASSIFICATION NUMBER: 03-APP-11CATION NUMBER: 05-APP-11CATION NUMBER: APPLICATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50018
TELEPHONE: 610-407-0700
TELEPAX: 610-407-0701
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INFORMATION FOR SEQ ID NO:
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LENCTH: 1597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TACAAAACTAAGCAGCTGTCTGTGTTTGTGACAGCCCTGACCCCATAGGCCTGACATCCTC
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ThrProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeu
                                                              ValArgLeuArgValAlaTyrAlaProArgAspLeuValIleSerIleSerArgAspAsn
                                                                                                   GGCACCAGCCTCACCTGTCAGGTGACCTTGCCTGGGACCAGGTGTGACCACGACCAGGTACC
                                                                                                                                AspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThr
                                                                                                                                                                                      ThrLysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHis
                                                                                                                                                                                                                                   TGTAAGCAGGGGACACCCCCCATGATCTCCTGGATTGGGGGCCTCCGTGTCCTCCCCGGGC
                                                                                                                                                                                                                                                      PheGluGluCysProProProSerPheSerTrpThrGlyAlaAlaLeuSerSerGlnGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAAACAACCCAGACAGAGAAGTGCAGGCCAGAGACCCAGGGCCGATTCCAACTCCTTGGG
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Indels:
Gaps:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                  APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNI
TITLE OF INVENTION: Sialoadhesin
TITLE OF INVENTION: (SAF-2)
                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                 STATE: F
                                                                                                                                                   ZIP:
                                                                                                 COMPUTER:
                                                                                                                                                                                                  CITY:
FILING DATE: 1 CLASSIFICATION:
                             APPLICATION NUMBER:
                                                                                                                                                                                                STREET: P.O. BOX 980 CITY: VALLEY FORGE
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                                                                                               IBM Compatible
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Query Match:
DB:
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FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEPHONE: 610-407-0701
TELEX: 846169
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2900 base pairs
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                                                                                                                                                                                                                                                      TCATATTTCTTTCGGCTAGAGAGGAGGAAGCATGAAATGGAGTTACAAATCACAGTTGAAT
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                 ThrLysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHis
                                                               TGTAAGCAGGGGACACCCCCCATGATCTCCTGGATTGGGGGCCTCCGTGTCCTCCCCGGGC
                                                                               PheGluGluCysProProProSerPheSerTrpThrGlyAlaAlaLeuSerSerGlnGly ::::::
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Matches:
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Sequence 1, Application US/09046736

Patent No. 6090582

GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
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                                                                                                                                                                                                                                                                                                                                   CCCCCAGGATCGCTCTCTTTGGTATGGCCAAAGTCACTTCCTCGTCTCCTCCTTCCC
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Best Local Similarity:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1501 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: (
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/046,736
FILING DATE: 24-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
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APPLICATION NUMBER: 60/0.
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
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                                          TACTTCTTTCGTATGGAGAAAGGAAAT---ATAAAATGGAATTATAAATATGACCAGCTC
                                                                                                                    ProAlaLysGlyAsnCysSerLeuValIleArgAspAlaGlnMetGlnAspGluSerGln
                                                                                                                                                              AACAACCCAGCTTGGGCAGTGCAGGAGGAAACTCGGGACCGATTCCACCTCCTTGGGGAC
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                           ProGlyValArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAla 507
                                                          GGCCTGGCTGCCCACTCCTCAGGGGAGGAAAGAGAGATCCAGTATGCACCCCTCAGCTTT
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### Pamily Member-3  ### Pamil		· · · · · · · · ·
Tamily Member-3  Tamily		
Tamilly Member-3  2 mailly Membe		21PheTrpTleArgValGlnGluSerValMetValProGluGlyLeu 35
Pamily Member-3  Pamily	TACACAGGCAAAATGAGGCCTGTATCAGGAGTGTTGCTG	SerGlnalaMetAspGlyArg 20 ::: ::::::::::::::::::::::::::::::::
Tamily Member-3  Tamily		09-937-636-3 (1-512) x US-09-046-736-3 (1-1502)
Samily Member-3  Pamily		21.18% Indels: 166 3 Gaps: 10
### Pamilly Member-3    Pamilly Member-3   Pamilly		1502   156 11ve: 63
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200 200 200 200 200 200 200 200 200 200		CO
22		TELEX: INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
2		TELECOMMUNICATION INFORMATION: TELEPHONE: 610-407-0701 TELEFAX: 610-407-0701
Pamily Member-3  Pamily Member 3  Pamily		REGISTRATION NUMBER: 23,031 REFERENCE/DOCKET NUMBER: GH-50019
2 76 76 76 76 76 76 76 76 76 76 76 76 76	512	ATTORNEY/AGENT INFORMATION:
2 200 200 200 200 200 200 200 200 200 2		PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/041,885
2		APPLICATION NUMBER: US/09/046,736 FILING DATE: 24-MAR-1998 CLASSIFICATION: 514
29amily Member-3 29amily Member - 3 29amily Member	512	SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
Qy 76 Db 318 Qy 96 Db 378 Db 378 Qy 116 Db 438 Qy 136 Db 438 Db 495 Db 512		COMPUTER: IDM Compatible OPERATING SYSTEM: DOS
. Qy 76 Db 318 Qy 96 Db 378 Qy 96 Db 378 Qy 116 Db 438 Qy 136 Db 495	512	COMPUTER READABLE FORM:
. Qy 76 Db 318 Qy 96 Db 378 Db 438 Qy 136 Db 438		STATE: PA COUNTRY: USA
. Qy 76 Db 318 Qy 96 Db 378 Db 378 Db 378 Qy 116 Db 438 Qy 136		STREET: P.O. Box 980 CITY: Valley Forge
. Qy 76 Db 318 Qy 96 Db 378 Db 378 Db 438		CORRESPONDENCE ADDRESS: ADDRESSEE: Ratner & Prestia
. Qy 76 Db 318 Qy 96 Db 378		TITLE OF INVENTION: Staloadhesin Family Member-3 NUMBER OF SEQUENCES: 4
. Qy 76 Db 318 Qy 96 Db 378		APPLICANT: KIKLY, KRISTINE APPLICANT: ERICKSON-MILLER, CONNIE
76 318		Sequence 3, Application US/09046736 Patent No. 6090582 GENERAL INFORMATION:
76		
200		Db 1406 GAGATCAAG 1414 . Qy
258	258 GTTCATGGCTACTGGTTCCGGGCAGGGAATGATATAAGCTGGAAGGCTCCAGTGGCCACA	Qy 508 GluValLys 510 Db

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-09-937-636-3 (1-512) x US-09-620-312D-407 (1-1488)
                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (146)..(931)
US-09-620-312D-407
                                                                                                                                                                                                                                                                                                                         APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Aci
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
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SOFTWARE: Pt_Ft_genes Version
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GENERAL INFORMATION:
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Wang, Jian-Rui
Zhou, Ping
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Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
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Zhang, Jie
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                                              SerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSerProSerGln 313
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                                                                                                                                           GATGTCTCCTCATCCAGTTCCTCCACAGTCTGAATGGCCCATGTTTCTTCTTCATTGCTGG 1019
                                                                                                                                                                           AsnLeuGlyAsnGlyThrSerLeuProVal-----
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                                                                                                          ---LeuGluGlyGlnSerLeuCysLeu-----
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                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/027,974
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/760,031
FILING DATE: 13-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/274,107
FILING DATE: 21-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICANT: Barnett, Thomas;
APPLICANT: Kretschmer, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10591-314-COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: APPLE MACINTOSH 6500
COMPUTER: SYSTEM: SYSTEM 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: APPLE MACINTOSH
OPERATING SYSTEM: SYSTEM 7
SOFTWARE: WORDPETECT 3.5
CURRENT APPLICATION DATA:
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                 REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 242.10-KGB
TELECOMMUNICATION INFORMATION:
                                                             FILING DATE: 13-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: KUIT G. BI15COE
                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/207,678 FILING DATE: 16-JUN-1988 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 660 White CITY: Tarrytown STATE: New York
                                                                                                                                                                                                   APPLICATION NUMBER: US 07/060,031 FILING DATE: 19-JUN-1987
                                                                                                                                                    APPLICATION NUMBER: US 07/016,683 FILING DATE: 19-FEB-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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   (914) 332-1700
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                                                                                                                    US 06/896,361
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Best Local Similarity:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1339 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
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                                                   ---AGGCTGCAGCTGTCCAATGGCAACAGGACCCTCACTCTACTCAGTGTCACAAGGAAT
                                                                                                                    GACACAACCTACCTGTGGTGGATAAACAATCAGAGCCTCCCGGTCAGTCCC------
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GENERAL INFORMATION:
                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Sprung Horn Kramer &
STREET: 660 White Plains Road
                                                                                            TITLE OF INVENTION:
                                                                            NUMBER OF SEQUENCES:
                                                                                                                        APPLICANT: Barnett, Thomas; Elting, James; Kamarck, Michael; APPLICANT: Kretschmer, Axel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 242.9-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 13-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 21-NOV-1988
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: APPLE MACI
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 0
FILING DATE: 19-JUN-1987
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APPLICATION NUMBER:
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CLASSIFICATION: 435
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                                                                          GTTCTTCTCCTTGTCCACAATCTGCCCCAGCAA
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19-FEB-1987
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13-AUG-1986
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358 LeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThr 374	754 CCAGTCACCTTGAATGTCACCTATGGCCCGGACACCCCATTCCCCTTCAGACACC 813  283GlyGlnSerLeuCysLeuValCysValThrHisSerSerProproAla 298		77 HisGinSerArgGluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96 :::   :::::
APPLICATION NUMBER: US 07/207,678 FILLING DATE: 16-UNI-1988 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/060,031 FILLING DATE: 19-UNI-1987 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/016,683 FILLING DATE: 19-FEB-1987 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 06/896,361 FILLING DATE: 19-FEB-1986 ATTORNEY/AGENT INFORMATION: NAME: Kurt G. Briscoe REGISTRATION NUMBER: 33,141	NTOSH 6500 STEM 7.5 A: US/08/468,8568 1995 US 08/027,974 1993 US 07/760,031 1991 US 07/274,107 1988	RESULT B US-08-468-856B-2 US-08-468-856B-2 ; Sequence 2, Application US/08468856B ; Patent No. 6013772 ; GENERAL INFORMATION:     APPLICANT: Barnett, Thomas; Elting, James; Kamarck, Michael;     APPLICANT: Kretschmer, Axel     TITLE OF INVENTION: CDNAS CODING FOR MEMBERS OF THE     TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY     NUMBER OF SEQUENCES: 14     CORRESPONDENCE ADDRESS:     ADDRESSEE: Sprung Horn Kramer & Woods     STREET: 660 White Plains Road     CITY: Tarrytown     STATE: New York     COUNTRY: USA     COMPUTER READABLE FORM:     MEDIUM TYPE: Diskette, 3.50 inch, 2.0 Mb storage	

242.10-KGB

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEPAX: (914) 332-1844
INFORMATION: FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1630 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
640
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                            ValArgLeuArgValAlaTyrAlaProArgAspLeu---ValIleSerIleSerArgAsp
                                                           GACACAACCTACCTGTGGTGGATAAACAATCAGAGCCTCCCGGTCAGTCCC------
                                                                                      AspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThr
                                                                                                                      TCCAACCCTGTGGAGGACAAGGATGCTGTG----GCCTTCACCTGTGAACCTGAGACTCAG
                                                                                                                                                                                  --- CCGGAGCTGCCCAAGCCCTCC--
                                                                                                                                                                                                             PheGluGluCysProProProSerPheSerTrpThrGlyAlaAlaLeuSerSerGlnGly
                                                                                                                                                                                                                                                                          IleProGluThrLeuGluProGlyGlnProValThrValIleCysValPheAsnTrpAla
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AGGCTGCAGCTGTCCAATGGCAACAGGACCCTCACTCTACTCAGTGTCACAAGGAAT
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Matches:
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US-08-468-859A-2
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                                                                                                                                       ACCAACTTCAGCCTCCCCATCCCTAACAGCCACAGAAATAATTTATTCAGAAGTAAAAAA
                                                                                                                                                                                                    TAACAAGATGAATGAAGTTACTTATTCTACCCTGAACTTTGAAGCCCAGCAACCCACACA
                                                                                                                                                                                                                                                                                                                          GGGGCCATTGCTGGCATTGTGATTGGAGTAGTGGCCCTGGTTGCTCTGATAGCAGTAGCC
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ntsmatches: Indels: Gaps: 168-859A-2 (1-1630) LeuGlyGlySerGlnAlaMet         TA	TOPOLOGY: linear US-08-468-859A-2 Alignment Scores: Pred. No.: Score: Score: 187.00 Percent Similarity: 36.258 Conservative: 86 Conservative: 86	C TEC OF	PRIOR APPLICATION DATA:  APPLICATION NUMBER: US 07/016,683  FILING DATE: 19-FEB-1987  PRIOR APPLICATION DATA:  APPLICATION NUMBER: US 06/896,361  FILING DATE: 13-AUG-1986  ATTORREY_AGENT INFORMATION:  NAME: Kurt G. Briscoe	PRIOR APPLICATION DATA:  PRIOR APPLICATION DATA:  APPLICATION NUMBER: US 07/274,107  FILING DATE: 21-NOV-1988  PRIOR APPLICATION DATA:  APPLICATION NUMBER: US 07/207,678  FILING DATE: 16-JUN-1988  PRIOR APPLICATION DATA:  APPLICATION NUMBER: US 07/060,031  FILING DATE: 19-JUN-1987	APPLICATION NUMBER: US/08/468,859A FILING DATE: 06-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/027,974 FILING DATE: 08-MAR-1993 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/760,031	US SADA	GENERAL INFORMATION:  APPLICANT: Barnett, Thomas; Elting, James; Kamarck, Michael;  APPLICANT: Kretschmer, Axel  TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY  NUMBER OF SEQUENCES: 14  CORRESPONDENCE ADDRESS:  ADDRESSEE: Sprung Horn Kramer & Woods  STREET: 660 White Plains Road  CITY: Tarrytown  STATE: New York
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Qy Qy	ор Оу Оу Ор	Db Db	0y 0y 0y	ОУ ОУ ОУ	0y 0y 0b	0
319 ValleuGluLeuProArgValGlnValGluHisGluGlyGluPheThrCysHisAlaArg 338	283GlyGlnSerLeuCysLeuValCysValThrHisSerSerProProAla 298	640AGGCTGCAGCTGTCCAATGGCAACAGGACCCTCACTCTACTCAGTGTCACAAGGAAT 696  249 ASNThrProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr 267  :::   697 GACACAGGACCCTATGAGTGTGAAATACAGAACCCCAGTGAGTGCGAACCGCAGTGAC 753  268ValLeuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGlu 282	532 TCCAACCCTGTGGAGGACAAGGATGCTGTGGCCTTCACCTGTGAACCTGAGACCTCAG 588  210 AspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaglnArgThr 229	IleProGluThrLeuGluProGlyGlnProValThrValIleCysValPheAsnTrpAla	MetGlnAspGluSerGlnTyrPhePheArgValGluArgGlySerTyrValArgTyrAsn	77 HisGlnSerArgGluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96 :::   :::::	163 CCCACCACTGCCCAGCTCACTACTGAATCCATGCCATTCAATGTTGCAGAGGGGAAGGAG 222 41

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RESULT 10
US-08-468-856B-1
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       APPLICATION UNMBER: US/08/468,856B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/027,974
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quence 1, Application US/08468856B
tent No. 6013772
                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10591-5144
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                       STREET: 000
CITY: Tarrytown
CTTY: New York
                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                        MEDIUM TYPE: Diskette, 3.50 inc
COMPUTER: APPLE MACINTOSH 6500
OPERATING SYSTEM: SYSTEM 7.5
SOFTWARE: WOIGEPAFFECT 3.5
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                         E: Sprung Horn Kramer & Woods
660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                               Barnett, Thomas; Elting, James; Kamarck, Michael; Kretschmer, Axel
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US 07/760,031
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE SHARACTERISTICS:
SEQUENCE SHARACTERISTICS:
SEQUENCE SHARACTERISTICS:
1.7. 1.7. 1.1.
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REFERENCE/DOCKET NUMBER: MD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 13-AUG-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/016,683 FILING DATE: 19-FEB-1987 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 21-NOV-1988
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STRANDEDNESS: single
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                                       130 PheMetAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLysProAspValTyr 149
                                                                                  412
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         457 CTTGTGAATGAA--
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                                                                                                             MetGlnAspGluSerGlnTyrPhePheArgValGluArgGlySerTyrValArgTyrAsn 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaLysGly----
                                                                                                                                                                                                                          ----AACCGTCAAATTGTAGGATATGCAATAGGAACTCAACAAGCTACCCCAGGGCCC
                                                                                                                                                                                                                                                                                                                                                                     GTTCTTCTCCTTGTCCACAATCTGCCCCAGCAA---
                                                                              CAGAATGACACAGAATTCTACACCCTACAAGTC
                                                                                                                                                    GCAAACAGCGGTCGAGAGACAATATACCCCCAATGCATCCCTGCTGATCCAGAACGTCACC
                                                                                                                                                                                                                                                         {\tt HisGlnSerArgGluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro}
                                                                                                                                                                                                                                                                                             GGCTACAGCTGGTACAAAGGG-----GAAAGAGTGGATGGC------
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCACCACTGCCCAGCTCACTACTGAATCCATGCCATTCAATGTTGCAGAGGGGAAGGAG 222
                                                                                                                                                                                                                                                                                                                                                                                                      -----CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyr
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19-JUN-1987
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ProGlyValArgPro---ArgProGluAlaArgMetProLys-----GlyThrGlnAla 504
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                                                                                                                                                    SerLysLysAsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSer 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGTTGCTCTG---ATAGCAGTAGCCCTGGCATGTTTTCTGCATTTCGGGAAGACCGGC 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeu------
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                                                                                                                                                                                                                                              GlnLysAlaThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGlu 447
                                                                                                                                                                                                                                                                                          CAG-----GACCACTCCAAT----- 1230
                                                                                                                                                                                                                                                                                                                              ThrIleLeuAspTyrIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsn 427
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                                                                               ThrGlnAlaProGluSerGlnGluSerGlnGluLeuHisTyrAlaThrLeuAsnPhe 487
                                                                                                                            AACAAGATGAAT-----
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                                        Alignment Scores: Pred. No.:
                                                                                                       US-08-468-859A-1
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  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Applic Patent No. 6022958
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                                                                                                                                                                                                                             TELEFAX: (914) 332-18 INFORMATION FOR SEQ ID NO:
                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 3173 nucleotides
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Barnett, Thomas; APPLICANT: Kretschmer, Axel
                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 13-AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US OF FILING DATE: 19-FEB-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19-JU
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                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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SYSTEM: SYSTEM 7.5
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914) 332-1844
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Matches:
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300 LeuSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGlyVal 319	283GlyGlnSerLeuCysLeuValCysValThrHisSerSerProProAlaArg 299	268 ValleuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGlu 282	249 AsnThrProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr 267 :::	230 ValArgLeuArgValAlaTyrAlaProArgAspLeuValIleSerIleSerArgAsp 248           :::::::   :::   ::::   :::	210 AspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThr 229	190 ThrLysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHis 209 :::	170 PheGluGluCysProProProSerPheSerTrpThrGlyAlaAlaLeuSerSerGlnGly 189	150 IleProGluThrLeuGluProGlyGlnProValThrValIleCysValPheAsnTrpAla 169	130 PheMetAsnAspGlyPhePheLeuLySValThrAlaLeuThrGlnLySProAspValTyr 149 :::   :::	110 MetGlnAspGluSerGlnTyrFhePheArgValGluArgGlySerTyrValArgTyrAsn 129	97 AlaLysGly	77 HisGlnSerArgGluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96 ::::  ::::::	58 GlyTyrTrpPheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsn 76 	41CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyr 57 :::    :::   223 GTTCTTCTCCTTGTCCACAATCTGCCCCAGCAACTTTTT 261	25 ValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro	5 LeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArgPheTrpIleArg 24 	DB: US-09-937-636-3 (1-512) x US-08-468-859A-1 (1-3173)	21 009 Wigneytobes.
; FILING DATE: 06-0UN-1995; CLASSIFICATION: 424; PRIOR APPLICATION DATA: papelication NUMBER: US 08/027,974	OPERATING SYST	COMPUTER: APPLE MEDICATION OF THE COMPUTER OF	CITY: Tarrytown STATE: New York COUNTRY: USA 7TB: 10501-5144	NUMBER CORRES ADDR	CANT: Barnett, CANT: Kretschme OF INVENTION: OF INVENTION:	RESULT 12 IS-08-468-8 Sequence Patent No	Qy 505 AspTyrAlaGluValLysPheGln 512	Qy 488 ProGlyValArgProArgProGluAlaArgMetProLysGlyThrGlnAla 504 :::    :::    :::     Db 1279 GAAGCCCAGCAACCCACCAACCTTCAGCCTCCCCTAACAGCCACAGAAATA 1338	Oy 468 ThrGinAlaProGluSerGlnGluSerGlnGlucluLeuHisTyrAlaThrLeuAsnPhe 487	1240	428 GINLYSALATNIPIOASNSerProArgThiProLeuProPioGlyAlaProSerProGlu 1231GACCCACCT	408 ThrileLeuAspTyrileAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsn	Db 1159 AGGCAAGCGACCAGCGTGATCTCACAGAGCACAAACCCTCAGTCTCCAACACACT 1215	3/6 LeuLeuPheLeuCysLeuAlaIeuIleIleMetLysIleLeu	1042		320 LeuGluLeuProArgValGlnValGluHisGluGlyGluPheThrCysHisAlaArgHis	

130 PheMetAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLysProAspValTyr	Qy 110 MetGlnAspGluSerGlnTyrPhePheArgValGluArgGlySerTyrValArgTyrAsn 129	352 GCAAACAGCGGTCGAGAGACAATATACCCCAATGCATCCCTGCTGATCCAGAACGTCACC	Oy 97 AlaLysGlyANDESTANDANTAIDEANTAIDEANTAIDEANTAIDEATABDAIGIN 109	77 HisGinSerArgGluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro ::::   ::::::	Qy 58 GlyTyrTrpPheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsn 76	Db 223 GTTCTTCTCCTTGTCCACAATCTGCCCCAGCAACTTTTT 261	41CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyr	Qy 25 ValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40 :::       ::: ::    Db 163 CCCACCACTGCCAGCTCACTACTGAATCCATGCCATTCAATGTTGCAGAGGGAAGGAG 222	Qy 5 LeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArgPheTrpIleArg 24        :::            Db 127 CTGCTCACAGCCTCACTTCTAACCTTCTGGAACCCG 162	US-09-937-636-3 (1-512) x US-08-468-856B-6 (1-3461)	6.84% Indels: 3 Gaps:	Pred. No.: 1.2e-07 Length: 3461 Score: 185.00 Matches: 130 Percent Similarity: 34.65% Conservative: 80 Best Local Similarity: 21.45% Mismatches: 200		ESS:	SEQUENCE CHARACTERISTICS: LENGTH: 3461 nucleotide	e . 00 10 <b>N</b> :	ATTUREY/AGENT INFORMATION:  NAME: KURT G. BETISCOE  REGISTRATION NUMBER: 33,141  REFERENCE/DOCKET NUMBER: MDI 242.10-KGB	APPLICATION N FILING DATE:	PR.					; PRICE APPLICATION UMBER: US 07/274,107		FILING DATE: 08-MAR-PRIOR APPLICATION DATA:
Qy 442 GlyAla	QY 422 LeuAlaGinLysargAsnGinLysalaThrepasnsereroargThrepolereroero 441	1240 GATGCTGGGACGTATTGGTGTGAGGTCTTCAACCCAATCAGTAAGAACCAAAGCGACCCC	Qy 418	Db 1183 AGGATGAAGCTGTCCCAGGGCAACACCACCCTCAGCATAAACCCTGTCAAGAGGGAG 1239	1123 AATGACACTGGAATCTCCATCGGTTGTTCTTCAAAAACCAGAGTCTCCCGTCCTCGGAG	Db 1078 ACAGTCACAGGAGATAAGGACTCTGTGAACCTGACCTGCTCCACA 1122 Ov 383 LeuIleIleMetLysIleLeuProLysArgArgThrGlnThrGluThrPro 399	Qy 365AsnGlyAlaPheLeuGlyIleGlyIleThrAlaLeuLeuPheLeuCysLeuAla 382	Db 1018 ATCATAGTCACTGAGCTAAGTCCAGTAGTAGCAAAGCCCCAAATCAAAGCCAGCAAGACC 1077	979 AACTCAGTCACTGCCTGCAACAGGACCACAGTCAAGACG			Qy 299 ArgieuSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGly 318 :::        Db 874 CAGTACTCCTGGCTTATCAATGGAACATTCCAGCAAAGCACAAGAG 921	814 TATTACCGTCCA	GlyGlnSerLeuCysLeuValCysValThrHisSerSerProProAla	Qy 268ValLeuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGlu 282	Qy 249 AsnThrProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr 267 :::	Qy 230 ValargleuargValalaTyralaProArgAspLeuValileSerIleSerArgAsp 248         :::::::    ::::	589 GACACAACCTACCTGTGGTGGATAAACAATCAGAGCCTCCCGGTCAGTCCC	Qy 210 AspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThr 229	Db 532 TCCACCCCTGTGGAGGACAAGGATGCTGTGGCCTTCACCTGTGAACCTGAGACTCAG 588	Qy 190 ThrLysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHis 209	Db 496CCGGAGCTGCCCAAGCCCTCCATCTCCCAGCAACAAC 531	Qy 170 PheGluGluCysProProProSerPheSerTrpThrGlyAlaAlaLeuSerSerGlnGly 189	Db 495 495	Qy 150 IleProGluThrLeuGluProGlyGlnProValThrValIleCysValPheAsnTrpAla 169	Db 457 CTTGTGAATGAAGAAGCAACTGGACAGTTCCATGTATAC 495

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RESULT 13
US-08-468-859A-6
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                                                   APPLICATION NUMBER: US 07/016,683
FILING DATE: 19-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/896,361
FILING DATE: 13-AUG-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                            PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/016,683
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STREET: VCC
CITY: Tarrytown
CTATE: New York
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APPLICATION NUMBER: 19-JUN-
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                                                                                                                                                                                                                APPLICATION NUMBER: US 07 FILING DATE: 16-JUN-1988
                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 21-NOV-1988
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/760,031 FILING DATE: 13-SEP-1991
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0: FILING DATE: 08-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/468,859A FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
         REFERENCE/DOCKET NUMBER:
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SYSTEM: SYSTEM 7.5
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DB:
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TELEPHONE: (914) 332-1700
TELEPAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                          AlaGluValLysPheGln 512
                                                                                                                 CAGCAACCCACAACCAACTTCAGCCTCCCCATCCCTAACAGCCACAGAAATAATTTAT
                                                                                                                                           ValArgPro--ArgProGluAlaArgMetProLys-----GlyThrGlnAlaAspTyr 506
                                                                                                                                                                                             TCCAATGACCCACCTAACAAGATGAATGAAGTTACTTATTCTACCCTGAACTTTGAAGCC
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US-08-408-095-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-937-636-3 (1-512) x US-08-408-095-30 (1-2166)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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LENGTH: 2166 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30,951
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK &
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chinnadurai, Govindaswamy
TITLE OF INVENTION: APOPTOPSIS-REGULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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STREET: 2100 Pen
CITY: Washington
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              116 rPhePheArgValGluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePh 136
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Mack, Susan J.
Mack Susan J.
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510 76T	431 hrProAsnSerProArgThrProLeuProProGlyAlaProSerProGluSerL	Qy
439 GGGACCCTTAGCTGGCACTTAGAT	1193 AAGGCCCCACTCCCTGGGATGCTACAATCCAATGGAAGATGGCATTAGCTACACCA 1252	DЬ
170	411	Qy
176 Brogorbhogormandulougonch	1133 ATTCCAGCGGCCAGAGCTTCTTTGTGAGGAATAAAAAGGTTAGAAGGGCCCCCCCTCTCTG 1192	Db
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	1073	Db
348 CGAGTCTACCAGATTCCTGGGAAG	2y 389 LeuProLysArgArgThrGlnThrGluThr 398	Qу
138	1025	В
303 GCAACTAA	<pre>2y 369 euGlyIleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIle- 388 :: :::   ::: :::                      </pre>	Qy
120	983	Ф
243	<pre>2y 350LeuSerValHisTyrLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheL 369</pre>	Qy
100 As	923 CGGGTGCCTACTGGTGCCAGGGGACCAACAGTGTGGGCAAGGGCCGTTCGCCTCTCAGCA 982	Db
937-636-3 (1-512)	330	Qy
ch:	868	뫄
Percent Similarity: 33.95% Best Local Similarity: 23.33%	2y 310 erProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGluHisG 330	Qy
	821	Db
Alignment Scores.	294 erSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuS 310	Qy
ORGANISM: Murine	775 -	Db
; LENGTH: 1348	274 snGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCysValThrHisS 294	Qy
ARE: PatentIn Ver	Db 774 774	Db
_ FE F	254 roGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGluAsnLeuGlyA 274	Qy
RENCE: 0575	728	DЬ
일임	Qy 234 alAlaTyrAlaProArgAspLeuValIleSerIleSerArgAspAsnThrProAspProP 254	Qy
APPLICANT: Van, Shi Du	671	Db
Stern, Da	2) 214 hrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThrValArgLeuArgV 234	Qy
~ z (	622AGCCAGCTGAATTTTGACTCCATCTCCCCAGAA-GATGCTGGGAGTTACA 670	DЬ
US-09-638-649-6	194	Qy
د	Db 579 CCAGTTCTTCTGGGAGAAAAATGGCAGGCTTCTGGGGAAAGAA 621	Db
1 4 5 1	176 oSerPheSerTrpThrGlyAlaAlaLeuSerSerG	Qy
1411	Db 525 TGGAAACTCGGTCAGCCTCCAATGTGACTTCTCAAGCAGCCACCCCAAAGAAGT 578	Дb
471 roGluSerGinGluSe	156	Qy
1373	496	Db
453	136 еLе	Qy
	Db 495 495	Дb

Db	Qy	Qу	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	US-09-93	Alignment Pred. No.: Score: Percent Si Best Local Query Matc	RESULT 15 US-09-638-649 Sequence 6, Patent No. PATENT P	Qy Db	Db V	Qy Db
	203 ThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSerArg 221	192ProThrThrSerHispheSerValLeuSerPhe 202	176 ProSerPheSerTrpThrGlyAlaAlaLeuSerSerGlnGlyThrLys 191 :::	157 GlyGlnProValThrValIleCysValPheAsnTrpAlaPheGluGluCysProPro 175	138 LysValThrAlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluPro 156 :::	120 ValGluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeu 137            :::    ::: 303 GCAACTAACAGGCGAAGGAGGTCAAGTCCAACTACCGA	SSerLeuVallleArgAspAla       ::::: TTCCCTCCTCCTTCCAGCCACT	7-636-3 (1-512) x US-09-638-649-6 (1-1348)	Alignment Scores: 4.24e-07 Length: 1348 Pred. No.: 172.50 Matches: 101 Score: 172.50 Matches: 101 Percent Similarity: 33.95% Conservative: 46 Best Local Similarity: 23.33% Mismatches: 139 Query Match: 4 Gaps: 21	SULT 15 :-09-538-649-6 :-09-638-649-6 :-09-638-649-6 :-09-638-649-6 :-09-638-649-6 :-09-638-649-6 :-09-638-649-6 :-09-638-649-6 :-09-638-649-6 :-09-638-649-6 :-09-638-649-6	491 rgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLys 510	4/1 TOGETGERGERGERGERGERGERGERGERGERGERGERGERGERG	ysLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAlaP

	ted: October 8, 2003, 22:42:57 9 secs	Search completed: Oc Job time : 139 secs	Jo
		1170	В
	ProGlyValArgProArgProGluAlaArgMetProLys 500	488	δ
1169	GCCCCGGAAAGCCAGGAGGATGAAGGAGGAACGTGCAGAGCTGAAT	1125	밁
487		468	δ
1124	G -	1116	망
467	ysLysAsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSer 	448	δ
1115	CCCAGGCGTGAG	1101	밁
447	GlnLysAlaThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGlu	428	Ş
1100	GTCGGGGCTATCCTGTGGCGAAAACGA	1074	밁
427		408	δ
1073		1073	DЬ
407	${\tt IleLeuProLysArgArgThrGlnThrGluThrProArgProArgPheSerArgHisSer}$	388	ο
1073	CTGGGAGGCCTGGGAGTAGTAGCCCTGCTC	1044	망
387	heLeuCysLeuAlaLeuIleIleMetLys	368	Ş
1043	CCAGCTGAAGGCTCTGTGGGTGAGTCTGGGCTGGGCTAGCCCTGGCCTTGGGGATC	984	망
367		355	δ
983	CACGGACCTCAGGAAAGCCCTCCTGTCAGCATCAGGGTCACAGAAACCGGCGATGAGGGG	924	망
354		342	δō
923		864	В
341	LeuProArgValGlnValGluHisGluGlyGluPheThrCysHisAlaArgHisProLeu	322	δ
863	TGGATAAAGGATGGTGCACCCTTGCCCCTGGCTCCCAGCCCTGTGCTGCTC	813	Вb
321	ProGlyValLeuGlu	302	δ
812	CCTGGTGGGACTGTGACCTTGACCTGTGCCATCTCTGCCCAGCCCCCTCCTCAGGTCCAC	753	Вþ
301	er	282	δ
752	GAGCCTGAAGGTGGAATAGTCGCT	729	밁
281	SerGlnAlaAsnArgThrValLeuGluAsnLeuGlyAsnGlyThrSerLeuProValLeu	262	Ş
728	CGAGTCAGGGAGCCTGGGCCTCCAGAGGGCATTCAGCTGTTGGTT	684	В
261		242	Q
683		636	밁
241	alSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAspLeu	222	ð

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Sequence Sequence

27, 148, 1, A, 258, 258,

Sequence Sequence

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Result
No.
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-OP-Cgn2_1/USPTO_spool/US09937636/runat_08102003_083237_24/app_query.fasta_1.711
-OB-Published_Applications_NA -OFMT-fastap -SUFFIX-p2n.rnpb -MINNATCH-0.1
-LOOPEL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pc -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-200000000 -USER-US0937635_eCGN_pl_1271_@runat_08102003_083237_24
-NCPU-6 -ICPU-3 -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100
-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5
-FGAPOP-6 -FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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2706
                                                                        Query
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                                            Description
  Sequence 15, Appl
                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/910,600
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/220,139
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 2208
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-910-600-15
; Sequence 15, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:
Alignment Scores: Pred. No.: Score:
                                                                                            ; ORGANISM: Homo US-09-910-600-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
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APPLICANT: Chang, Han
APPLICANT: Whitney, Gena
TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
FILE REFERENCE: D0003NP
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252	Qy 252 252  Db 1018 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGGATTCAGGGCGC 1077	958 CAGCCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCCTCCCATCCC 10	Db 898 GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGACAGC 957  Qy 252 252		Qy 241 LeuVallleSerIleSerArgAspAsnThrProAsp 252	Qy 221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240	Qy 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220	Qy 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200	Qy 161 ThrvallleCysValPheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp 180	Db 538 GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACCCTGGAGCCCGGGCAGCCGGTG 597	478 GAGAGAGCTATGTGAGATATATTCATGAACGATGGGTTCTTCTAAAAGTAACA 53	TCACAGTACTTCTTI GlvPhePheLeuLvs	101 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal	Qy 81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 100	yAlaProValAlaThrAsnHisGln              TGCTCCTGTGGCCACAAACCACCAG	Qy 41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60	Qy 21 PheTrpIleArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40	Qy 1 MetLeuLeuProLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20 	1001: 95.36% Index: 11 Gaps: 17-636-3 (1-512) x US-09-910-600-15 (1-2208)	Percent Similarity: 73.31% Conservative: 1 Best Local Similarity: 73.17% Mismatches: 1
Qy 496 AlaargMetProLysGlyThrGlnAlaAspTyrAlaGluValLysPheGln 512		2038 T	456 TyrGlnLeuProSerPheProGluProLysSerSerThrGlnAlaProGluSerGlnGlu 4	Qy 436 ArgThrProLeuProProGlyAlaProSerProGluSerLysLysAsnGlnLysLysGln 455	410 VALFICTHER LAGLYFECHENTAGLHLYSALGASHGEHLYSALGASHGELTLY 43	396 TATGIUTAPPROAGPPROSEGRAFINSSETHRILLELEUASPTYRILLEUASPTYRILL	1798 CITCTTTTCCTCTGCCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGACGGACTCAG	1730 Lyberty went reserving and the control of the	1678 TGTGAGGCCTGGAACGTCCATGGGGCCCCAGAGTGGATCCATCC	Db 1618 CCCTGGGCCAACAGCTCCCTGAGCCTCCATGGAGGGCTCAGCTCCGGCCTCAGGCTCCGC 1677	Db 1558 GAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCTCAGCCGGG 1617  Qy 354 354	Qy 354 354	Db 1498 CACTGCAGCTGCTCCCAGGCCAGCCCGGCCCCTCTCTGCGCTGGTGGCTTGGGGAG 1557	331 SERVALHISTYE	331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu	11 ProSerGinProSerAspProGlyValLeuGinLeuProArgValGinValGiuHisGiu 	1258 GTCACACAGCCCCCCAGCCTGAGCTGAGCCCAGAGGGGACAGGTTCTGAGC	201 ValThr#1sSerSorProDroAlaArglenSerTrpThrGlnArgGlvGlnVallenSer	$\frac{253}{1138}$	1078 TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTGTG

	B Q B Q B Q B Q B Q B Q B Q B Q B Q B Q	181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200	101 THE VALUE OF STATE OF THE AST	49 GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACCCTGGAGCCCGGGCAGCCGGTG	141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 160	121 GIUAEGGIYSETTYTVAIAEGTYTASHTNEMECASHASPGIYFNEPHELEULYSVAITHT 140	23 19C1CC119919A1CA9A9AC9C9CA9A19CA9A19A9TCACA11CTCTTCTTCTG1g15 4	101 CysserLeuvalIleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 120 	GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAAGGGAAAC 4	81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 1 	309 TTCANAGCAGTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA 368	CTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG	CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 6	21 PheTrpIleArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40	1 MECLEULEUFFOLEULEUSEFSETLEULEUGTYSTYSETGIALAMETASPGIYATG 20 	-3 (1-512) x US-09-910-600-27 (1-3024)	11 Gaps:	Mismatches:	7.71e-253 2580.50	Alignment Scores:	OTHER INFORMATION: Description of Artificial Sequence: L3-995-2	ORGANISM: Artificial Sequence FEATURE:	TYPE: DNA	IWARE: PatentIn Ver. 2.0	DR FILING DATE: 2000-07-21 BER OF SEQ ID NOS: 32	CURRENT APPLICATION NUMBER: US/09/910,600  PRIOR APPLICATION NUMBER: 60/220,139	FILE REFERENCE: DO003NP FILE REFERENCE: D0003NP FILE REFERENCE: D0003NP	STOLEGS AND HOES	APPLICANT: Longphre, Malinda	Publication No. US20030036631A1
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OTHER INFORMATION:

or

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FITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PF489P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 69/836,353
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2000-04-19
PRIOR FILING DATE: 2000-04-19
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US-09-984-130-148
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                                                                                                                                            LENGTH: 2338

TYPE: DNA

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:

PAME/KEY: SITE
LOCATION: (3)

OTHER INFORMATION: n equ
NAME/KEY: SITE
LOCATION: (6)

OTHER INFORMATION: n equ
                                                                                                                                                                                                                                                                                        SOFTWARE: Pa
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                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR FILING DATE: 1998-10-28
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 149
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NAME/KEY:
LOCATION:
                                                                                                       NAME/KEY: SITE
LOCATION: (9)
OTHER INFORMATION: n
                                                                  OTHER INFORMATION:
                                                                             NAME/KEY: SITE LOCATION: (11)
                           OTHER INFORMATION:
                                      NAME/KEY: SITE LOCATION: (12)
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                                                                                                                                                                                                                                                                                                      PatentIn Ver.
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PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg

TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA

440 80 380 60 320 40 260 20

CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC PheTrpI1eArgValGlnGluSerValMetValProGluGlyLeuCySI1eSerValPro

TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCCAGCTTATGGCTACTGG

381

В 20 뭥 QΥ 밁

321

41

261

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Percent Similarity:
Best Local Similarity:
Query Match:
                 Qy
                                                                                                          Alignment Scores: Pred. No.:
                                                                                                                                       ; NAME/KEY: SITE
; LOCATION: (38)
; OTHER INFORMATION:
US-09-984-130-148
                                      US-09-937-636-3 (1-512) x US-09-984-130-148 (1-2338)
                                                                                                                                                                                                                                                                            LOCATION: (31)
OTHER INFORMATION: R
NAME/KEY: SITE
LOCATION: (32)
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LOCATION: (23)
OTHER INFORMATION: (25)
NAME/KEY: SITE
LOCATION: (25)
OTHER INFORMATION: (26)
NAME/KEY: SITE
LOCATION: (26)
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LOCATION: (29)
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Conservative:
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Indels:
Gaps:
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291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310	TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCTGGACCTCTCTGTGProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu [	GTCCCATACCTGGAAGCCCAAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCTGACAGC CAGCCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCCTCCATCCC TGGGGCCCTAGACCCCTGGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC	201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220	141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 160	81 GluValGluMetSerThrArgGlyArgPheglnLeuThrGlyAspProAlaLysGlyAsn 100
REFERENCE: D0003NP WY APPLICATION NUMBER: US/09/910,600 WY APPLICATION NUMBER: 60/220,139 APPLICATION NUMBER: 60/220,139 FILING DATE: 2000-07-21 ROF SEQ ID NOS: 32 RE: PatentIn Ver. 2.0 NO 1 H: 2565 : DNA VISM: Homo sapiens		2061 C- 456 T- 2121 T- 2181 A- 2181 A-	Oy  Oy  Oy  Oy  IIIIIIIIIIIIIIIIIIIIIII	354	351 SerValHisTyr

Oy 252 252	Db 795 CAGCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCCCATCCC 854	Qy 252 252	Db 735 GTCCCATACCTGGAAGCCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCTGACAGC 794	Qy 252 252	Qy 241 LeuValIleSerIleSerArgAspAsnThrProAsp 252	Qy 221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240	Db 555 AGCTTCACGCCCAGGACCCCAGGACCACACACACCCTACCTGCCATGTGGACTTCTCC 614	201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer	Qy 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200          549	Db 548 548	Qy 161 ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp 180	Db 548 548	409 GRURNSKURRIGUERIGI GRURNIA I RATITI CATIGAAK GATIGGGTTCTTTUTAARAGTAACA	121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 14 	Qy 101 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 120		81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 1	Qy 61 PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80	Qy 41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60 	Qy 21 PheTrpILeArgYa1GlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40	129 ATBCTACTBCTGCTGCTGCTGCTGGGGGGTCCCAGGCTATGGATGGAAGA	1 MetLeuLeuProLeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg	i-3 (1-512) x US-09-910-600	84.18%	22/8.00 Matches: 45 arity: 75.25% Constructive: 1 milarity: 75.08% Micmatches: 1	t Scores: 4.24e-222 Length:	
; APPLICANT: Eaton, Dan ApplicanT: Ferrara, Napoleon	Botstein, D	T: Ashkenazi, Av	S20020156006A1	295A-258	1755 TTCCAA 1	1695 511	ArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLys 5	471 ProGluSerGlnGluSerGlnGluGluLeuHiSTyrAlaThrLeuAsnPheProGlyVal		151	431 ThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGluSerLystys 450	Db 1455 GATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGAAAGCC 1514	Qy 411 AspTyrIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla 430	Qy 391 LysArgArgThrGluThrPtoArgProArgPheSerArgHisSerThrIleLeu 410	1335 ATCGGCATCACGGCTCTTTTCCTCTGCCTGGCCTGATCATCATGAAGATTCTACCG	Db 1275 TCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGA 1334	SerValHisTyrLysLysClyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly	Db 1215 GGAGAGTTCACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGTCTCTCTC	311 ProserGinProserAsperGinYvalLeuGinLeuProArgyvalGinValGinIssiu	1095 GTCACACAGCAGCCCCCCAGCCAGGCTGACCCAGAGGGGACCAGAGGTTCTGAGC	Qy 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310	QY 271 ASDLEUGLYASNGLYTHTSETLEUPTOVALLEUGLUGLYGLNSETLEUCYSLEUVALCYS 290	Db 975 CAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTCCTGGAA 1034	Qy 253ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270	Db 915 TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCCAGCAGCGAGCCCTGGACCTCTCTGTG 974	Qy 252 252	Db 855 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC 914

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FILE REFERENCE: P2630PICII

CURRENT APPLICATION NUMBER: US/09/978,295A

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/06249

PRIOR FILING DATE: 1997-11-30

PRIOR PRIOR APPLICATION NUMBER: 60/06311

PRIOR APPLICATION NUMBER: 60/06311

PRIOR APPLICATION NUMBER: 60/06364

PRIOR PILING DATE: 1997-11-31

PRIOR PRIOR FILING DATE: 1997-11-21

PRIOR PRIOR PRICING NUMBER: 60/077450

PRIOR PRICING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR APPLICATION NUMBER: 60/077641

PRIOR PRICING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR PRICING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR PRICING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                         OR APPLICATION NUMBER: 60/07804
OR FILING DATE: 1998-03-13
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078930
OR APPLICATION NUMBER: 60/078930
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079656
OR FILING DATE: 1998-03-26
OR APPLICATION NUMBER: 60/079664
OR APPLICATION NUMBER: 60/079663
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/0797663
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079728
OR APPLICATION NUMBER: 60/079728
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079920
OR FILING DATE: 1998-03-30
OR APPLICATION NUMBER: 60/079920
OR FILING DATE: 1998-03-30
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Williams, P. Mickey
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Fong, Sherman
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OR APPLICATION NUMBER: 60/082804
OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082700
OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082797
OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082796
OR FILING DATE: 1998-04-23
OR APPLICATION NUMBER: 60/083336
OR FILING DATE: 1998-04-27
OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-29
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OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083558
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083559
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OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/081838
OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/082568
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082569
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082704
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DR FILLING DATE: 1998-03-31
DR APPLICATION NUMBER: 60/080107
DR FILLING DATE: 1998-03-31
DR APPLICATION NUMBER: 60/080165
DR FILLING DATE: 1998-03-31
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R APPLICATION NUMBER: 6
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APPLICATION NUMBER: 60/081229
FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955
FILING DATE: 1998-04-15
FILING DATE: 1998-04-15
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FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
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FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/080334
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Db 286 CHILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Alignment Scores:  Pred. No.:  9.93e-221  Score:  9.93e-221  Matches: 450  Matches: 450  Percent Similarity: 74.928  Ouservative: 1  Best Local Similarity: 74.758  Mismatches: 3  Query Match: 10  Qy 1 MetLeuLeuProLeuLeuLeuSerSerLeuLeuGyGlySerGlnAlaMetAspGlyArg DB:  US-09-937-636-3 (1-512) x US-09-978-295A-258 (1-2764)  Qy 1 MetLeuLeuProLeuLeuLeuSerSerLeuLeuGyGlySerGlnAlaMetAspGlyArg Db 46 ANGCTACTGCCACTGCTGCTGCTGCTGGTGGGCGGTCCCAGGCTATGGATGG	RIOR APPLICA RIOR FILING RIOR
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APPLICANT:
APPLICANT:
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: PA53091C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
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Hillan, Kenneth J
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OR FILING DATE: 1998-03-26
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079664
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079663
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079728
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OR APPLICATION NUMBER: 60/079728
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OR APPLICATION NUMBER: 60/07978
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079920
OR APPLICATION NUMBER: 60/079923
OR FILING DATE: 1998-03-30
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OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/078004
OR FILING DATE: 1998-03-13
OR APPLICATION NUMBER: 60/078886
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078910
OR APPLICATION NUMBER: 60/078910
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DR FILING DATE: 1997-10-17
DR APPLICATION NUMBER: 60/064249
DR FILING DATE: 1997-11-03
DR APPLICATION NUMBER: 60/065311
DR FILING DATE: 1997-11-13
DR FILING DATE: 1998-04-08
DR APPLICATION NUMBER: 60/081071
DR FILING DATE: 1998-04-08
DR APPLICATION NUMBER: 60/081195
DR FILING DATE: 1998-04-08
DR APPLICATION NUMBER: 60/081203
DR FILING DATE: 1998-04-09
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PR APPLICATION NUMBER: 60/080327

PR FILING DATE: 1998-04-01

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PR APPLICATION NUMBER: 60/080333

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PR FILING DATE: 1998-04-01
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Percent Similarity:
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FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085582
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APPLICATION NUMBER: 60/085700
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{\tt ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp}
                                  SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer|
                                                                                  ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu
                                                                                                                                                                                                                         GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr
                                                                                                                                                                                                                                                        TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG
                                                                                                                                                                                                                                                                    CysSerLeuValIleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 120
                                                                                                                                                                                                                                                                                                                   GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn
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                                                                                                                                      {\tt ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProSerPheSerTrp}
                                                                                                                                                                                     AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal
                                                                                                                                                                                                            GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC
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OR APPLICATION NUMBER: 60/083496
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083499
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083545
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/08354
OR APPLICATION NUMBER: 60/083554
OR APPLICATION NUMBER: 60/083558

APPLICATION NUMBER: 60/ FILING DATE: 1998-04-29

60/083495

APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083392 FILING DATE: 1998-04-29

APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-27 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-23

60/082796

FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082700
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APPLICATION NUMBER: 60/082797
APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22

APPLICATION NUMBER: 6: FILING DATE: 1998-04-

FILING DATE: 1998-04-21 APPLICATION NUMBER:

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60/082704

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FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/

60/082804

FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-15

60/081838

APPLICATION NUMBER: 60/ FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/

60/081952

60/081819

FILING DATE: 1998-04-APPLICATION NUMBER: 60/

1998-04-09

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R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/08
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DR APPLICATION NUMBER: 60/083742
DR FILING DATE: 1998-04-30
DR APPLICATION NUMBER: 60/084366
DR FILING DATE: 1998-05-05
DR APPLICATION NUMBER: 60/084414
DR FILING DATE: 1998-05-06
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60/084600 60/084598 60/084640

APPLICATION NUMBER: 60/ FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/

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CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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OR FILING DATE: 1997-11-03
OR APPLICATION NUMBER: 60/065311
OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/066364
OR FILING DATE: 1997-11-21
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
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Hillan, Kenneth J
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Botstein, David
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APPLICATION NUMBER: 60/079920 FILING DATE: 1998-03-30 APPLICATION NUMBER: 60/079923

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APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079786
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APPLICATION NUMBER: 60/079663 FILING DATE: 1998-03-27

FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/ FILING DATE: 1998-03-31 APPLICATION NUMBER:

60/080165 60/080107

60/080194

APPLICATION NUMBER: 60/ FILING DATE: 1998-03-31

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-09-937-636-3 (1-512) x US-09-978-192A-258 (1-2764)
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APPLICATION NUMBER: 60/083392
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APPLICATION NUMBER: 60/083495
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DR APPLICATION NUMBER: 60/081955
DR FILING DATE: 1998-04-15
DR APPLICATION NUMBER: 60/081817
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60/082796 60/082797 60/082700 60/082804 60/082704 60/082569 60/082568 DR APPLICATION NUMBER: 60/081049
DR FILING DATE: 1998-04-08
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Kljavin, Ivar J
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Grimaldi, J. Christopher
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Gerritsen, Mary E
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Gao, Wei-Qiang
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APPLICANT:
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-0-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
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OR APPLICATION NUMBER: 60/065311
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
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Gao, Wei-Qiang
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Shelton, David L.
Stewart, Timothy A.
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Botstein, David
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OR APPLICATION NUMBER: 60/082804
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OR APPLICATION NUMBER: 60/084441
DR FILING DATE: 1998-05-06
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APPLICATION NUMBER: 60/084366 FILING DATE: 1998-05-05 APPLICATION NUMBER: 60/084414 FILING DATE: 1998-05-06

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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Feirara, Napoleon
APPLICANT: Feirara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Gao, Wei Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: KNO, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Paon, James;
APPLICANT: Paon, James;
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Applicant Polity Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C22
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Prior Application removed - See File Wrappes SEQ ID NO 258

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311 ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGluH1Glu 330		2 CAGCCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCTCT	GC - AT - GC	61 ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProSerPheSerTrp 65	121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140
APPLICANT: Tumas, Daniel APPLICANT: Williams, p. Mickey APPLICANT: Wood, William I.  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C15 CURRENT APPLICATION NUMBER: US/09/978,585A CURRENT FILING DATE: 2001-10-16 NUMBER OF SEQ ID NOS: 624 Prior Application removed - See File Wrapper or Palm SEQ ID NO 258 LENGTH: 2764 TYPE: DNA ORGANISM: Homo Sapiens US-09-978-585A-258	APPLICANT: Godowski, Paul J. APPLICANT: Grinaldi, J. Christopher APPLICANT: Grinaldi, J. Christopher APPLICANT: Gurney, Austin L. APPLICANT: Hillan, Kenneth J APPLICANT: Kljavin, Ivar J. APPLICANT: Kuo, Sophia S. APPLICANT: Napier, Mary A. APPLICANT: Pan, James; APPLICANT: Pan, James; APPLICANT: Roy, Margaret Ann APPLICANT: Shelton, David L. APPLICANT: Stewart, Timothy A.	APPLICANT: ASRKehazi, AVI  APPLICANT: Baker Kevin P.  APPLICANT: Betsein, David  APPLICANT: Besnoyers, Luc  APPLICANT: Eaton, Dan  APPLICANT: Ferrara, Napoleon  APPLICANT: Filvaroff, Ellen  APPLICANT: Fong, Sherman  APPLICANT: Gao, Wei-Qiang  APPLICANT: Gerrber, Hanspeter  APPLICANT: Gerrber, Mary E.  APPLICANT: Goddard, Audrey	Argeroarge:	431 ThrProAssSerProArgThrProLeuProProGlyAlaProSerProGluSerLysLys	Oy 391 LysargArgThrGlnThrGlnThrFroArgProArgPheSerArgHisSerThrIleLeu 410

Db 772 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC 831	712 CAGCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCCCATCCC 77	Oy 252 252	Db 652 GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGGCTCCTCTGTGCTGCTGACAGC 711	ОУ 252 252		241 LeuVallleSerlleSerArqAspAsnThrProAsp	Qy 221 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240 	OY 201 SerbheThrProArgProGlnAspH1sAspThrAspLeuThrCysH1sValAspPheSer 220	466GTGCTC 4	Qy 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200		Qy 161 ThrVallleCysValPheAsnTrpAlaPheGluGluCysProProSerPheSerTrp 180		Qy 141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 160	Qy 121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140	Db 346 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 405	Qy 101 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 120	286 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCCAAGGGGAAC 3	81 GluValGluMetSerThrArqGlyArqPheGlnLeuThrGlyAspProAlaLysGlyAsn 10	Qy 61 PhelysalaValThrCluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80	σ	4	106 TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC 1	Qy 21 PheTrpIleArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40		1 MetLeuLeuProLeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyAr	·937-636-3 (1-512) x US-09-978-585A-258 (1-2764)	83.70% Indels:	t Similarity: 74.92% Conservative: 1 Cocal Similarity: 74.75% Mismatches: 3	gnment Scores: 9.93e-221 Length:
; APPLICANT: EATON, DAN ; APPLICANT: Ferrara, Napoleon ; APPLICANT: Filvaroff, Ellen	APPLICANT: Botste	APPLICANT: A	equence	191A-258	1672 T	Qy 511 PheGln 512	OY 491 AFGYFOAFGYFOGIUALAKGMECFFOLYSGLYTHIGIHALAKSPTYFALGGLUVALLYS 310	1552 CCAGAATCCCAGGAGAGCCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTC	471 ProGluSerGlnGluSerGlnGluGluLeuHisTyrAlaThrLeuAsnPheProGlyVal	Qy 451 AsnolnLysLysGlnTyrcInLeubroSerPheProGluProLysSerSerThrGlnAla 470	1432 ACACCAAACAGTCCTCGGACCCCTCCTCCACCAGGTGCTCCCCCAGAATCAAAGAAG	431 ThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGluSerLysLys	GATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGAAAGCC	411 AspTyrIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla		391 LysArgArgThrGlnThrGluThrProArgProArgPheSerArgHisSerThrIleLeu	OY 3/1 11eGLY11eFinfAlaleuLeuPheLeuCySLeuAlaleu11e11eMeELyS11eLeuPfO 390	1192 TCGTGCACTATAAGAAGGGAACTCATCTCAACGGCATTCTCGGGA	Qy 351 SerValHisTyrLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370		331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu	Oy 311 ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGluHisGlu 330	1012 GTCACACAGCAGCCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGGACAGGTTCTGAGC	291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer	952 AACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTGGTCTGT	Qy 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCys 290	Db 892 CAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCCAAGCAAACAGGACAGTCCTGGAA 951	Qy 253ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270	Db 832 TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTG 891	QУ 252 252

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CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/06311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06364
PRIOR APPLICATION NUMBER: 60/07450
PRIOR FILING DATE: 1997-11-21
PRIOR PRIOR FILING DATE: 1998-03-10
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PRIOR APPLICATION NUMBER: 60/077631
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PRIOR APPLICATION NUMBER: 60/077641
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OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/078004
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OR APPLICATION NUMBER: 60/079689
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079663
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079728
OR FILING DATE: 1998-03-27
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OR FILING DATE: 1998-03-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
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Goddard, Audrey
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Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fong,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Daniel
ms, P. Mickey
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PRIOR
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OR APPLICATION NUMBER: 60/083392
OR FILING DATE: 1998-04-29
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OR APPLICATION NUMBER: 60/082704
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OR APPLICATION NUMBER: 60/083558
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083559
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083500
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DR FILING DATE: 1998-04-15

R APPLICATION NUMBER: 60/08

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DR APPLICATION NUMBER: 60/08

R FILING DATE: 1998-04-15
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FILING DATE: 1998-03-31
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FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/081070
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FILING DATE: 1998-04-01
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FILING DATE: 1998-03-31
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81 GluvalGlumetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 1	Qy 61 PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80	Qy 41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60	Qy 21 PheTrpileArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40	ProLeuLeuLeuSerSerLeuLeuG                     CACTGCTGCTGCTCGCTGCTGG	83.70% Indets: 11 Gaps: 2) x US-09-978-191A-258 (1-2764)	nt Similarity: 74.92% Conservative: 1 Local Similarity: 74.75% Mismatches: 3	Length:	; PRIOR FILING DATE: 1998-05-15; PRIOR APPLICATION NUMBER: 60/085697	FILING DATE	FILING DATE: 1998-05-1: APPLICATION NUMBER: 60,	FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08558	FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08557	FILING DATE: 1998-05-19 APPLICATION NUMBER: 60, FILING DATE: 1998-05-19 APPLICATION NUMBER: 60,	3 /08532 3 /08558			FILING DATE: 1998-05-0 APPLICATION NUMBER: 60 FILING DATE: 1998-05-0	FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/	FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/08464	APPLICATION NUMBER: 60/06463 APPLICATION NUMBER: 60/08463	APPLICATION NUMBER: 60/0844 FILING DATE: 1998-05-06 ADDITCATION NUMBER: 60/0846	; PRIOR FILING DATE: 1998-05-05; PRIOR APPLICATION NUMBER: 60/084414; PRIOR FILING DATE: 1998-05-06	1998-0 NUMBER:	FILING DATE
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351 SerValHisTyrLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370 	331 GlyGluPheThrCysH.sA.laArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350 	ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGluH1sGlu 3	291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310	AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCys	253ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270	32 TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTG	52	252	712 CAGCCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCCCATCCC 771	252 252	652 GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCCTCCTGTGCTGCTGACAGC 711	252 252	241 LeuVallleSerIleSerArgAspAsnThrProAsp	221 ArgLysG1yValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240 	201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220	181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200		161 ThrVallleCysValPheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp 180	465 465	141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 160	121 GHRATGGLYSGTTYTVALATGTTYFASH PROMETSASPGLYPROFINELGHLYSVALTHE 140	46 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGAGTGAGT	101 CysSerLeuValIleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 120	286 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC 345

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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Shelton, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT APPLICATION NUMBER: 00/918585
PRIOR APPLICATION NUMBER: 00/918585
PRIOR APPLICATION NUMBER: 60/082250
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US-09-978-403A-258
; Sequence 258, Application US/09978403A
; Sequence 100 No. US20030050240A1
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APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, Davi
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Gao, Wei-Qiang
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Gerritsen, Mary E.
Goddard, Audrey
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Botstein, David
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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                                                                                                                                                                                                                                                                                                                                                                                      Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                           James;
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                                                                                                                                                                                                                                                                                                        Nicholas F.
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OR FILING DATE: 1998-04-01
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OR APPLICATION NUMBER: 60/079786
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OR FILING DATE: 1998-03-27
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OR APPLICATION NUMBER: 60/078004
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OR APPLICATION NUMBER: 60/078936
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R APPLICATION NUMBER: 60/664249

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OR APPLICATION NUMBER: 60/085582
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OR APPLICATION NUMBER: 60/085573
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                                                    SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer
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                                                                                                                   ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu
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; PRIOR APPLICATION NUMBER: 60/078939 ; PRIOR FILING DATE: 1998-03-20 ; PRIOR APPLICATION NUMBER: 60/079294	PRIOR APPLICATION NUMBER: 60/078936  PRIOR FILING DATE: 1998-03-20  PRIOR APPLICATION NUMBER: 60/078910  PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/078004  PRIOR FILING DATE: 1998-03-13  PRIOR APPLICATION NUMBER: 60/078886  PRIOR PTILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/077649  PRIOR FILING DATE: 1998-03-11  PRIOR FILING DATE: 1998-03-7791  PRIOR FILING DATE: 1008-03-12	PRIOR APPLICATION NUMBER: 60/077641  PRIOR EFILING DATE: 1998-03-11  PRIOR EFILING DATE: 1098-03-11  PRIOR EFILING DATE: 1008-03-11	PRIOR APPLICATION NUMBER: 60/066364  PRIOR FILING DATE: 1997:11-21  PRIOR PRIOR PRIOR NUMBER: 60/077450  PRIOR PRIOR DATE: 1098-03-10	PRIOR APPLICATION NUMBER: 60/064249  PRIOR FILING DATE: 1997-11-03  PRIOR APPLICATION NUMBER: 60/065311  PRIOR PRIOR DATE: 1007-11-13	PRIOR APPLICATION NUMBER: 09/918585  PRIOR FILING DATE: 2001-07-30  PRIOR ETILING DATE: 1007/062250  PRIOR ETILING DATE: 1007/10/17	TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C25 CURRENT APPLICATION NUMBER: US/09/978,564A	APPLICANT: Williams; P. Mickey APPLICANT: Williams; P. Mickey APPLICANT: Wood, William I. FITTE OR INVENTION. Secreted and Transmembrane Delimentides and Nucleic	APPLICANT: Fan, Jounes APPLICANT: Paoni, Nicholas F. APPLICANT: Roy, Margaret Ann APPLICANT: Shelton, David L. APPLICANT: Stewart Timorthy A	APPLICANT: Kljavin, Ivar J.  APPLICANT: Kuo, Sophia S.  APPLICANT: Napier, Mary A.  APPLICANT: Par Targes	; APPLICANT: Godowski, Paul J. ; APPLICANT: Grimaldi, J. Christopher ; APPLICANT: Gurney, Austin L. · ADDITCANT: Uillan Kennoth T	APPLICANT: Gerber, Hanspeter APPLICANT: Gerritsen, Mary E. APPLICANT: Goddard, Audrey	Filvaroff Fong, She Gao, Wei-			tion INF	NEOULI 14   US-09-978-564A-258   Sequence 258, Application US/09978564A	1672 TTCCAA	Qy 511 PheGin 512 .

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DR FILING DATE: 1998-04-28
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OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/081838
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OR APPLICATION NUMBER: 60/082568
OR FILING DATE: 1998-04-21
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APPLICATION NUMBER: 60/080105
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APPLICATION NUMBER: 60/079656
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Percent Similarity:
Best Local Similarity:
Query Match:
DB: 9.93e-221 2265.00 74.92% 74.75% 83.70% Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

US-09-937-636-3 (1-512) x US-09-978-564A-258 (1-2764)

MetLeuLeuProLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20

Score:

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: Hillan, Kennern J : Kljavin, Ivar J : Kuo, Sophia S.	: Grimaldi, J. Christopher : Grimay, Austin L. : Grimay, Austin L.	Goddard, Aud Godowski, Pa	: Gerber, Hanspeter : Gerritsen, Mary E.	: Fong, Sherman : Gao, Wei-Qiang	Filvar	Eaton, Da	Botstein, D	Ash	os, Application US/0999833A n No. US20030054405A1 FORMATION:	A-258	2 TTCCAA 1677		AGACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAG		ProGluSerGlnGluSerGlnGluGluLeuHisTyrAlaThrLeuAsnPheProGlyVal	AACCAGAAAAAGCAGTATCAGTTTCCCAGAACCCAAATCATCCACTCAAGCC	AsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAla 470	2 ACACCAAACAGTCCTCGGACCCCTCCTCCACCAGGTGCTCCCTCC		SPITAL AND TO THE ALECT OF THE ALGOLITH AND THE ALGOLITH ALGO	Acountry 1   Observation   Wal Droffbrall act   vDrof   on all act   vI-vocatorate   vocatorate   vocatorate	L LYSAIGATGITTIGITTITTIGITTITTITATGETTITTITTITTITTITTITTITTITTITTITTITTITTI	ATCGGCATCACGGCTCTTCTTTTCCTCTGCCTGGCCCTGATCATCATGAAGATTCTACCG	1 IleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuPro 390		1 SerValHisTyrLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370	Calysturies in Cyshishiant ynts florewordyselvet in the Various flore to the Various flore			1 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310	2 AACCTTGGGAACGGCACGTCTCCCCAGTACTGGAGGGCCAAAGCCTGTGCCTGGTCTGT 1011

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141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 16	121 GluargGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 1 	101 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 	ω L	PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 8	41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60 	Qy 21 PheTrpIleArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40 	Metreureureureureuserserteureureureureureureureureureureureureure	tch: 83.70% Indels: 11 Gaps: 7-636-3 (1-532) Wis-DO-000-0322-356 (1-3764)	Percent Similarity: 74.92% Conservative: 1  Best Local Similarity: 74.75% Mismatches: 3	9.93e-221 Length:	Allonment Scorpe.	PRIO	PRIO	PRIO	PRIO	PRIC	PRIOR FILING DATE: 1998-05-15  PRIOR FILING DATE: 1998-05-15  PRIOR FILING DATE: 1998-05-15	PRIO	PRIC	PRIC	PRIC	PRIC	PRIC	PRIC	PRIC	PRIC
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